

## **FIGURE 1**

ACTGCACCTCGGTTATCGATTGAATTCCCCGGGATCCTCTAGAGATCCCTCGACCTCGA  
CCCACCGCGTCCGGGCCGGAGCAGCACGCCGCAGGACCTGGAGCTCCGGCTCGTCTCCCG  
CAGCGCTACCCGCCATCGCCTGCCGCCGGGGCGCTGGGCTCCTGCCGCTTGCTG  
CTGCTGCCGCCGCCGGAGGCCAAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGCT  
GGTGGACAAGTTAACCAAGGGATGGTGGACACCGCAAAGAAGAACTTGGCGCGGGAAACA  
CGGCTTGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTGCCCTGCTGGAGATC  
CTGGAGGGCTGTGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA  
GCACCTGGAGGCCTGGTGGCTCAGCTGAAGAGCGAATATCCTGACTTATTGAGTGGTTT  
GTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCAGTGTCTCGCATGC  
CAGGGCGGATCCCAGAGGCCCTGCAGCGGAATGGCCACTGCAGCGAGATGGAGCAGACA  
GGCGACGGGTCTGCCGGTGCACATGGGTACCAGGGCCGCTGTGACTGACTGCATGG  
ACGGCTACTTCAGCTCGCTCCGAACGAGACCCACAGCATTGACAGCCTGTGACGAGTCC  
TGCAAGACGTGCTCGGCCCTGACCAACAGAGACTGCCGGAGTGTGAAGTGGCTGGGTGCT  
GGACGAGGGCGCTGTGGATGTGGACCGAGTGTGCGGCCAGCCGCTCCCTGCAGCGCTG  
CGCAGTTCTGTAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTGTGACTCCAGCTGTG  
GGCTGCACAGGGAAAGGCCAGGAAACTGTAAAGAGTGTATCTCTGGCTACGCAGGGAGCA  
CGGACAGTGTGCAGATGTGGACGAGTGCCTACTAGCAGAAAAACCTGTGTGAGGAAAAACG  
AAAATGCTACAATACTCCAGGGAGCTACGTCTGTGTGCTGACGGCTTCGAAGAAACG  
GAAGATGCCGTGTGCCGCCGGCAGAGGCTGAAGCCACAGAAGGAGAAAGCCGACACAGCT  
GCCCTCCCGCGAAGACCTGTAATGTGCCGGACTTACCCCTAAATTATTAGAAGGATGTCC  
CGTGGAAAATGTGGCCTGAGGATGCCGTCTGCAGTGGACAGCGGGAGAGGCTGC  
CTGCTCTCTAACGGTTGATTCTCATTTGCCCTAAACAGCTGCATTCTGGTTGTTCTTA  
AACAGACTTGTATATTTGATACAGTTCTTGTAAATAAAATTGACCATTGTAGGTAATCAGG  
AGGAAAAAAAGGGCGGCCGACTCTAGAGTGCACCTGCAGAAGC  
TTGCCGCCATGGCCCAACTGTTATTGCAGCTATAATGGTTACAAATAAGCAATAGCA  
TCACAAATTCAAAATAAGCATTTCAGCTAGTTGTGGTTGCTCAAAC  
ATCAATGTATCTTATCATGTCTGGATCGGGATTAATTCCGCGCAGCACCATGCCCTGAAAT  
AACCTCTGAAAGAGGAACCTGGTTAGGTACCTCTGAGGCGAAAGAACCGAGCTGTGGAATG  
TGTGTCAGTTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAGCAG  
ATCTCAATTAGTCAGCAACCCAGTTT

## **FIGURE 2**

><subunit 1 of 1, 353 aa, 0 stop

><MW: 38192, pI: 4.53, NX(S/T): 2

MRLPRRAALGLLPLLLLPPAPEAAKKPTPCHRGRGLVDKFNQGMVDTAKKNFGGGNTAEEKTLSKYESSEIRL  
LEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFCVKTLKVCCSPGTYGPDCLACQGGSQRPCSG  
NGHCSGDGSRQGDGSCRCHMGYQGPLCTDCMDGYFSSLRNETHSICTACDESCKTCSGLTNRDCGECEVGWLDE  
GACVDVDECAAEPPPCSAAQFCKNANGSYTCEECDSSCVGCTGEGPNCKECISGYAREHGQCADVDEC SLAEKT  
CVRKNENCYNTPGSYVCVCPDGFETEDACVPPAEEATEGESPTQLPSREDL

**Signal peptide:**

amino acids 1-24

**N-glycosylation sites.**

amino acids 190-194 and 251-255

**Glycosaminoglycan attachment sites.**

amino acids 149-153 and 155-159

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 26-30

**Casein kinase II phosphorylation sites.**

amino acids 58-62, 66-70, 86-90, 197-201, 210-214, 255-259, 295-299, 339-343  
and 349-353

**Tyrosine kinase phosphorylation site.**

amino acids 303-310

**N-myristoylation sites.**

amino acids 44-50, 54-60, 55-61, 81-87, 150-156, 158-164, 164-170, 252-258 and  
313-319

**Aspartic acid and asparagine hydroxylation site.**

amino acids 308-320

**EGF-like domain cysteine pattern signature.**

amino acids 166-178

**Leucine zipper pattern.**

amino acids 94-116

## **FIGURE 3**

CAGGTCCAAC TGCACCTCGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTC  
GACCTCGACCCACGCGTCCGCCAGGCCGGAGGCAGCGCCAGCGTCTAAACGGGAACA  
GCCCTGGCTGAGGGAGCTGCAGCGCAGCAGAGTATCTGACGGGCCAGGTTGCGTAGGTGCG  
GCACGAGGAGTTTCCCGCAGCGAGGAGGTCTGAGCAGC **ATGGCCCGGAGGAGCGCCTTC**  
CCTGCCGCCGCGCTCTGGCTCTGGAGCATCCTCCTGTGCCTGCTGCCACTGCCGGAGGC  
CGGGCCGCCGCAGGAGGAGGCCTGTACCTATGGATCGATGCTCACCAAGGAAAGAGTACTCA  
TAGGATTGAAGAAGATACTTGATTGTTCAGAGGGAAAATGGCACCTTACACATGAT  
TTCAGAAAAGCGCAACAGAGAATGCCAGCTATTCTGTCAATATCCATTCCATGAATTTCAC  
CTGGCAAGCTGCAGGGCAGGCAGAATACTTCTATGAATTCTGTCTTGCCTCCCTGGATA  
AAGGCATCATGGCAGATCCAACCGTCAATGTCCCTCTGCTGGAAACAGTGCCCTACAAGGCA  
TCAGTTGTTCAAGTTGGTTCCATGTCTTGGAAAACAGGATGGGGTGGCAGCATTGAAGT  
GGATGTGATTGTTATGAATTCTGAAGGAAACACCATTCTCAAACACACTCAAATGCTATCT  
TCTTAAACATGTCAACAAGCTGAGTCCCAGGGTGCAGAACATGGAGGCTTTGTAAT  
GAAAGACGCATCTGCGAGTGTCTGATGGTTCCACGGACCTCACTGTGAGAAAGCCCTTG  
TACCCACGATGTATGAATGGTGGACTTGTGACTCCTGGTTCTGCATCTGCCACCTG  
GATTCTATGGAGTGAAC TGTGACAAAGCAAACACTGCTCAACCACCTGCTTAATGGAGGGACC  
TGTTCTACCCCTGGAAAATGTATTGCCCTCCAGGACTAGAGGGAGAGCAGTGTGAAATCAG  
CAAATGCCACAACCTGCGAAATGGAGGTAAATGCATTGGTAAAAGCAAATGTAAGTGT  
CCAAAGGTTACCAAGGGAGACCTCTGTTCAAAGCCTGTCTGCAGCCTGGCTGTGGTCACAT  
GGAACCTGCCATGAACCAACAAATGCCAATGTCAAGAAGGTTGGCATGGAAGACACTGCAA  
TAAAAGGTACGAAGCCAGCCTCATACATGCCCTGAGGCCAGCAGCGCCAGCTCAGGCAGC  
ACACGCCCTCACTTAAAAGGCCGAGGAGCGGGATCCACCTGAATCCAATTACATCTGG  
**TGA**ACTCCGACATCTGAAACGTTTAAGTTACACCAAGTTCATAGCCTTGTAAACCTTCA  
TGTGTTGAATGTTCAAATAATGTTCAATTACACTTAAGAATACTGCCCTGAATTTCATTAGCT  
TCATTATAAAATCACTGAGCTGATATTACTCTTCTTTAAGTTCTAAGTACGTCTGTAG  
CATGATGGTATAGATTCTTCTGTTCACTGCTGGACAGATTTATATTATGTCAATTGA  
TCAGGTTAAAATTTCAGTGTAGTTGGCAGATATTCTAAAATTACAATGCAATTGTT  
GTCTGGGGCAGGGAACATCAGAAAGGTTAAATTGGGAAAAATGCGTAAGTCACAAGAAT  
TTGGATGGTCAGTTAATGTTGAAGTTACAGCATTTCAGATTATGTCAGATATTAGAT  
GTTGTTACATTTTAAAATTGCTCTTAATTTCAGACTCTAATACAATATATTGACC  
TTACCAATTCCAGAGATTCACTGTTAGTTAAAAAAATTACACTGTGGTAGTGGCATT  
AAACAATATAATATCTAAACACAATGAAATAGGAATATAATGTATGAACCTTGCAT  
TGGCTTGAAGCAATATAATATTGTAACAAAACACAGCTCTTACCTAATAAACATTTAT  
ACTGTTGTATGTATAAAATAAAGGTGCTGCTTAGTTTTGGAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAGGGCGGCCGCACTCTAGAGTCGACCTGCAGAAGCTTGGC  
GCCATGGCCCAACTTGTATTGCAGCTTATAATG

## **FIGURE 4**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33094
><subunit 1 of 1, 379 aa, 0 stop
><MW: 41528, pI: 7.97, NX(S/T): 2
MARRSAFPAAALWLWSILLCLLALRAEAGPPQEEESLYLWIDAHQARVLIGFEEDILIVSEGK
MAPFTHDFRKAQQRMPAIPVNIHSMNFTWQAAGQAEYFYEFSLRSLDKGIMADPTVNVPPLL
GTVPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTILQTPQNAIFFKTCQQAECPGGC
RNGGFCNERRICECPDGFHGPHEKALCTPRCMNGGLCVTPGFCICPPGFYGVNCDKANCST
TCFNGGTCFYPGKCICPPGLEGEQCEISKCPQPCRNGGKIGKSCKCCKSKGYQGDLCSPVVC
EPGCGAHGTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAEERRDP
PESNYIW
```

**Signal peptide:**

amino acids 1-28

**N-glycosylation site.**

amino acids 88-92, 245-249

**Casein kinase II phosphorylation site.**

amino acids 319-323

**Tyrosine kinase phosphorylation site.**

amino acids 370-378

**N-myristoylation sites.**

amino acids 184-190, 185-191, 189-195, 315-321

**ATP/GTP-binding site motif A (P-loop).**

amino acids 285-293

**EGF-like domain cysteine pattern signature.**

amino acids 198-210, 230-242, 262-274, 294-306, 326-338

## **FIGURE 5**

CGGACGCGTGGCGTCGGCGGTGCAGAGCCAGGAGGCCAGGAGGCCACC**ATGTGGCGATGTCCACTGGGGCTAC**  
TGCTGTTGCTGCCGCTGGCTGGCCACTTGGCTCTGGGTGCCACGAGGGTCGTGGCGCCGG  
GAGCTAGCACCGGGCTCGCACCTGCAGGGCATCCGGACGCCGGAGGCCGGTACTGCCAGGA  
GCAGGACCTGTGCTGCCGCGCGTGCAGCAGACTGTGCCCTGCCACCTGGCGCCATCT  
GTTACTGTGACCTCTTGCAACCGCACGGTCTCGACTGCTGCCCTGACTTCTGGGACTTC  
TGCCTCGCGTGCCACCCCCCTTCCCCGATCCAAGGATGTATGCATGGAGGTGCTATCTA  
TCCAGTCTTGGAACGTACTGGACAACGTAAACCGTTGCACCTGCAGGAGAACAGGCAGT  
GGCATGGTGGATCCAGACATGATCAAAGCCATCAACCAGGGCAACTATGGCTGGCAGGCTGG  
GAACACAGGCCCTCTGGGCATGACCCTGGATGAGGGCATTGCTACGCCTGGCACCA  
TCCGCCCATCTCCTCGGTATGAACATGCATGAAATTATACTAGTGCTGAACCCAGGGAG  
GTGCTTCCCACAGCCTCGAGGCCTCTGAGAACGTGGCCAACCTGATTGAGCCTCTGA  
CCAAGGCAACTGTGCAGGCTCTGGCCTCTCCACAGCAGCTGTGCATCCGATGTGTCT  
CAATCCATTCTCTGGGACACATGACGCCGTGCCTGTCGCCCCAGAACCTGCTGTGAC  
ACCCACCAGCAGCAGGGCTGCCCGTGGCGTCTCGATGGTGCCTGGTGGTCCCTGCGTCG  
CCGAGGGGTGGTGTCTGACCACTGCTACCCCTCTCGGGCGTGAACGAGACGGAGCTGGCC  
CTGCGCCCCCTGTATGATGCACAGCCGAGCCATGGTCGGGCAAGGCCAGGCCACTGCC  
CACTGCCCAACAGCTATGTTAAACAAATGACATCTACCAAGTCACTCCTGTCTACCGCCT  
CGGCTCCAACGACAAGGAGATCATGAAGGAGCTGATGGAGAACGGCCCTGTCAAGCCCTCA  
TGGAGGTGCATGAGGACTTCTTCCATACAGGGAGGCATCTACAGCCACAGCCAGTGAGC  
CTTGGGAGGCCAGAGAGATACGCCGGCATGGGACCCACTCAGTCAAGATCACAGGATGGGG  
AGAGGAGACGCTGCCAGATGGAAGGACGCTCAAATACTGGACTGCGCCAACCTGGGCC  
CAGCCTGGGGCGAGAGGGCCACTTCCGCATCGTGCAGCGTCAATGAGTGCAGATCGAG  
AGCTCGTGTGGCGTCTGGGCCTGGGCAGGGCATGGAGGACATGGGTCACTGAGGCTG  
CGGGCACCACGCCGGTCCGGCTGGATCCAGGCTAAGGGCGGGCGGAAGAGGCCCAATG  
GGCGGTGACCCAGCCTGCCGACAGAGGCCGGCGCAGGCCGGGCCAGGGCGCTAAT  
CCCGCGCGGGTTCCGCTGACGCAGGCCCGCTGGGAGGCCGGCAGGCCAGACTGGCG  
GAGCCCCAGACCTCCAGTGGGGACGGGGCAGGGCTGGGAGAGCACAGCTGCAG  
ATCCCAAGGCCCTGGGCCCTCAAGACTACCAAGGCAGGACACCTCAAGTCTCCAGC  
CCCAATAACCCACCCAAATCCGTATTCTTTTTTTTTAGACAGGGCTTGCTCCG  
TTGCCCAAGGTGGAGTGCAGTGCCTCAGGGCTCACTGTAACCTCCGACTCTGGTTCA  
AGTGAACCTCCACCTCAGCCTCTCAAGTAGCTGGACTACAGGTGCACCACACCTGGC  
TAATTTGTATTTGTAAAGAGGGGGTCTCACTGTGTTGCCAGGCTGGTTCGAACT  
CCTGGGCTCAAGCGGTCCACCTGCCTCCGCCTCCAAAGTGCTGGATTGCAGGCATGAGCC  
ACTGCACCCAGCCCTGTATTCTTATTCTCAGATATTATTTCTTCACTGTTAAAAA  
TAAAACCAAAGTATTGATAAAAAAAA

## **FIGURE 6**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33223
><subunit 1 of 1, 164 aa, 1 stop
><MW: 18359, pI: 7.45, NX(S/T): 1
MWRCPLGLLLLLPLAGHLALGAQQGRGRRELAPGLHLRGIRDAGGRYCQEQLCCRGRAADD
ALPYLGAICYCDLFCNRTVSDCCPDFWDFCLGVPPPFPIQGCMHGGRIYPVLGTYWDNCNR
CTCQENRQWHGGSRHDQSHQPGQLWLAGWEQRLLGHDPG
```

**N-glycosylation site.**

amino acids 78-82, 161-165

**Casein kinase II phosphorylation site.**

amino acids 80-84, 117-121, 126-130, 169-173, 205-209, 296-300,  
411-415

**N-myristoylation site.**

amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230,  
269-275, 378-384, 442-448

**Amidation site.**

amino acids 26-30, 318-322

**Eukaryotic thiol (cysteine) proteases histidine active site.**

amino acids 398-409

## **FIGURE 7**

AGGCTCCTTGGCCCTTTCCACAGCAAGCTTNTGCNATCCCGATTGTTGTCTCAAATCCA  
ATTCTCTTGGGACACATNACGCCCTGCTCCTTNGCCCCAGAACCTGCTGTCTGTACACCCAC  
CAGCAGCAGGGCTGCCCGNTGGCGTCTCGATGGTGCCTGGTGGTCTGCCTGCCGAGG  
GNTGGTGTCTGACCACTGCTACCCCTCTCGGGCCGTGAACGAGACGAGGCTGGCCCTGCGC  
CCCCCTGTATGATGCACAGCCGAGCCATGGTCGGGCAAGCGCCAGGCCACTGCCACTGC  
CCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACTCCTGTCTACCGCCTGGCTC  
CAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCATGGAGG  
TGCATGAGGACTTCTTCTTACAGGGAGGCATCTACAGCCACAGGCCAGTGAGCCTTGGG  
AGGCCAGAGAGATAACGCCGGCATGGACCCACTCAG

## **FIGURE 8**

GCTGCTTGCCTGTTGATGGCAGGCTTGCCTGCAGCCAGGCACTGCCCTGCTGTGCTACT  
CCTGCAAAGCCCAGGTGAGCAACGAGGATGACTGCCTGCAGGTGGAGAATGTCACCCAGCTGGGG  
GAGCAGTGCTGGACCCGCGCATCCGCGCAGTTGGCCTCCTGACCGTCATCAGCAAAGGCTG  
CAGCTTGAACTGCGTGGATGACTCACAGGACTACTACGTGGCAAGAAGAACATCACGTGCT  
GTGACACCGACTTGTGCAACGCCAGCGGGGCCATGCCCTGCAGCCGGCTGCCGCCATCCTT  
GCGCTGCTCCCTGCACTCGGCCTGCTGCTCTGGGACCCGCCAGCTATAGGCTCTGGGGGG  
CCCCGCTGCAGCCCACACTGGGTGTGGTCCCCCAGGCCTCTGTGCCACTCCTCACAGACCTG  
GCCCAGTGGAGCCTGTCCGTGGTCCCTGAGGCACATCCTAACGCAAGTCTGACCATGTTGT  
CTGCACCCCTGTCCCCCACCCGTACCCCTCCCATGCCCTCTCCAGGACTCCCACCCGGCAGA  
TCAGCTCTAGTGACACAGATCCGCCTGCAGATGGCCCTCCAACCCCTCTGCTGCTGTTTC  
CATGGCCCAGCATTCTCCACCCTTAACCCCTGTGCTCAGGCACCTCTCCCCCAGGAAGCCTT  
CCCTGCCACCCATCTATGACTTGAGCCAGGTCTGGTCCGTGGTGTCCCCCGCACCCAGCA  
GGGGACAGGCACTCAGGAGGGCCCAGTAAAGGGTGAGATGAAGTGGACTGAGTAGAAACTGGA  
GGACAAGAGTCGACGTGAGTTCCGTGGAGTCTCCAGAGATGGGCCTGGAGGCCTGGAGGAA  
GGGGCCAGGCCTCACATTCGTGGGCTCCCTGAATGGCAGCCTGAGCACAGCGTAGGCCCTT  
AATAAACACCTGTTGGATAAGCAAAAAAA

## **FIGURE 9**

MTHRTTWARRTSRAVTPTCATPAGPMPCSRLPPSLRCSLHSACCSDPASYRLWGAPLQPT  
LGVVPQASVPLLTDLAQWEPVLVPEAHPNASLTMYVCTPVPHDPPMALSRTPTRQISSLDT  
DPPADGPSNPLCCCFHGPAFSTLNTPVLRHLFPQEAFPAHPIYDLSQVWSVVSPAPSRGQALRRAQ

**Signal peptide:**

amino acids 1-47

**N-glycosylation site.**

amino acids 31-35, 74-78, 84-88

**Casein kinase II phosphorylation site.**

amino acids 22-26, 76-80

**N-myristoylation site.**

amino acids 56-60

**Amidation site.**

amino acids 70-74

## **FIGURE 10**

CCCATCGCGTCCGAACCTCTCCAGCGATGGGAGCCGCCGCCTGCTGCCAACCTCACTCTGT  
GCTTACAGCTGCTGATTCTCTGCTGTCAAACACTCAGTACGTGAGGGACCAGGGCGCCATGACC  
GACCAGCTGAGCAGGCCAGATCCGCGAGTACCAACTCTACAGCAGGACCAGTGGCAAGCA  
CGTGCAGGTACCGGGCGTCGCATCTCCGCCACCGCCGAGGACGGCAACAAGTTGCCAAGC  
TCATAGTGGAGACGGACACGTTGGCAGCCGGGTTCGCATCAAAGGGCTGAGAGTGAGAAG  
TACATCTGTATGAACAAGAGGGCAAGCTCATGGGAAGCCCAGCGGGAAAGAGCAAAGACTG  
CGTGTTCACGGAGATCGTGGAGAACAACTATA CGGCCTTCCAGAACGCCGGCACGAGG  
GCTGGTTCATGGCCTTCACGCCGCAGGGCGGCCAGGCTTCCGCAGGCCAGAAC  
CAGCGCGAGGCCCACTTCATCAAGGCCCTTACCAAGGCCAGCTGCCCTCCCCAACCACGC  
CGAGAAGCAGAAGCAGTTGAGTTGGCTCCGCCCCACCCGCCGACCAAGCGCACAC  
GGCGGCCAGCCCTCACGTAGTCTGGGAGGCAGGGGGCAGCAGGCCCTGGCCGCCTCCC  
CACCCCTTCCCTTAATCCAAGGACTGGCTGGGTGGCGGGAGGGGAGCCAGATCCCC  
GAGGGAGGACCCCTGAGGCCCGAAGCATCCGAGCCCCCAGCTGGGAAGGGCAGGCCGGTG  
CCCCAGGGCGGCTGGCACAGTGCCCTTCCGGACGGTGGCAGGCCCTGGAGAGGAAC  
GAGTGTCAACCTGATCTCAGGCCACCAGCCTCTGCCGCCCTCCAGCCGGCTCCTGAAGCC  
CGCTGAAAGGTCA CGCACTGAAGGCCTTG CAGACAACCGTCTGGAGGTGGCTGT CCTCAAAA  
TCTGCTTCTCGGATCTCCCTCAGTCTGCCCTTCCAGCCCCAAACTCCTCCTGGCTAGACTGTA  
GGAAGGGACTTTGTTGTTGTTGTTCAAGGAAAAAGAAAGGGAGAGAGAGGAAAATAG  
AGGGTTGTCCACTCCTCACATTCCACGACCCAGGCCTGCACCCACCCCCACTCCCAGCCC  
CGGAATAAAACCATTTCCTGC

## **FIGURE 11**

MGAARLLPNLTLCLQLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHKVQVTGRRI  
SATAEDGNKFAKLIVETDTFGSRVRIKGAESEKYICMNKRGKLIGKPSGKSKDCVFTEIVLE  
NNYTAFQNARHEGWFMAFTRQGRPRQASRSRQNQREAHFIKRLYQGQLPFPNHAEKQKQFEF  
VGSAPTRRTKRTRRPQPLT

**Signal peptide:**

amino acids 1-22

**N-glycosylation site.**

amino acids 9-13, 126-130

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 60-64

**Casein kinase II phosphorylation site.**

amino acids 65-69

**Tyrosine kinase phosphorylation site.**

amino acids 39-48, 89-97

**N-myristoylation site.**

amino acids 69-75, 188-194

**Amidation site.**

amino acids 58-62

**HBGF/FGF family signature.**

amino acids 103-128

## FIGURE 12

ACTTGCCATCACCTGTTGCCAGTGTGGAAAATTCTCCCTGTTGAATTTCGCACATGGAG  
GACAGCAGCAAAGAGGGCAACACAGGCTGATAAGACCAGAGACAGCAGGGAGATTATTTAC  
CATACGCCCTCAGGACGTTCCCTCTAGCTGGAGTTCTGGACTTCACAGAACCCATCCAGT  
CATTGATTGCTGTTATTCTTTCTTTCTCCACCATTTGATTTAT  
TTCCGTACTTCAGAAATGGGCTACAGACCACAAAGTGGCCCAGCCATGGGCTTTTCCT  
GAAGTCTTGGCTTATCATTCCCTGGGCCTACTCACAGGTGTCCAAACTCCTGGCCTGCC  
CTAGTGTGTGCCGCTGCGACAGGAACCTTGTCTACTGTAATGAGCGAAGCTGACCTCAGTG  
CCTCTGGGATCCCGAGGGCGTAACCGTACTCTACCTCCACAACAACCAAATTAATAATGC  
TGGATTCCTGCAGAACTGCACAATGTACAGTCGGTGACACGGTCTACCTGTATGGCAACC  
AACTGGACGAATTCCCCATGAACCTCCAAAGAATGTCAAGAGTTCTCCATTGCAGGAAAAC  
AATATTAGACCATTCACGGGCTGCTTGTGCCCAGCTTGAAGCTTGAAGAGCTGCACCT  
GGATGACAACCTCCATATCCACAGTGGGGTGGAAAGACGGGCCTCCGGGAGGGCTATTAGCC  
TCAAATTGTTGTTGTCTAAGAATCACCTGAGCAGTGTGCCTGTGGCTCCTGTGGAC  
TTGCAAGAGCTGAGAGTGGATGAAAATCGAATTGCTGTATATCCGACATGGCCTCCAGAA  
TCTCACGAGCTTGGAGCGTCTTATTGTGGACGGAACCTCCTGACCAACAAGGGTATGCCG  
AGGGCACCTTCAGCCATCTCACCAAGCTCAAGGAATTTCATAATTGTACGTAATTGCTGTCC  
CACCCCTCCTCCGATCTCCAGGTACGCATCTGATCAGGCTCTATTGCAGGACAACCAGAT  
AAACCACATTCTTGACAGCCTCTCAAATCTCGTAAGCTGGAACGGCTGGATATATCCA  
ACAACCAACTGCGGATGCTGACTCAAGGGTTTGATAATCTCTCAACCTGAAGCAGCTC  
ACTGCTCGGAATAACCCCTGGTTGTGACTGCAGTATTAAATGGGTACAGAATGGCTCAA  
ATATATCCCTTCATCTCTCACACGTGCGGGTTCATGTGCCAACGGTCTGAACAAGTCCGG  
GGATGGCGTCAGGGATTAAATGAATCTTGCTCTGTCCCACCACGACCCCCGGCCTG  
CCTCTCTCACCCAGCCCCAAGTACAGCTCTCCGACCACCTCAGCCTCCCACCCCTCTAT  
TCCAAACCTAGCAGAAGCTACACGCCTCCAACCTCCTACCACATCGAAACTTCCCACGATT  
CTGACTGGGATGGCAGAGAAAGAGTGACCCCACCTATTCTGAACGGATCCAGCTCTATC  
CATTGTTGATGACTTCAAGTCAGCTGGCTCTCTCTCACCCTGATGGCATA  
CAAACTCACATGGGTGAAATGGCCACAGTTAGTAGGGGCATCGTTAGGAGCGCATAG  
TCAGCGGTGAGAAGCAACACCTGAGCCTGGTTAACCTAGAGCCCCGATCCACCTATCGGATT  
TGTTAGTGCCACTGGATGCTTTAACCTACCGCGCGTAGAAGACACCAATTGTCAGAGGC  
CACCAACCATGCCTCTATCTGAACAACGGCAGCAACACAGCGTCCAGCCATGAGCAGACGA  
CGTCCCACAGCATGGCTCCCCCTTCTGCTGGCGGGCTTGTATGGGGGCGCGGTGATATT  
GTGCTGGTGGCTTGCTCAGCGTCTTGTGGCATATGCACAAAAAGGGCGCTACACCTC  
CCAGAAGTGGAAATACAACCGGGCGCGAACAGATGATTATGCGAGGCAGGCACCAAGA  
AGGACAACCTCCATCCTGGAGATGACAGAAACCGAGTTTCAGATCGTCTCCTTAATAACGAT  
CAACTCCTTAAAGGAGATTTCAGACTGCAGCCATTACACCCAAATGGGGCATTAATTA  
CACAGACTGCCATATCCCCAACACATGCGATACTGCAACAGCAGCGTGCCAGACCTGGAGC  
ACTGCCATACGTGACAGCCAGAGGCCAGCGTTATCAAGGCGGACAATTAGACTCTTGAGAA  
CACACTCGTGTGTCACATAAGACACGCAGATTACATTGATAATGTTACACAGATGCAT  
TTGTCATTTGAATACTCTGTAATTATACGGTGTACTATATAATGGGATTAAAAAGTG  
CTATCTTCTATTCAAGTTAACAGTTGTAACCTTGCTTTAAATCTT

## **FIGURE 13**

MGLQTTKWPISHGAFFLKS~~WLI~~ISLGLYSQVS~~KLLACPSVCRCDRN~~FVYC~~NERSLTSVPLGIP~~  
EGVT~~VLYLHNNQINNAGFPAELHNVQS~~VHTVYLYGNQLDEFPMNL~~PKNVRVLHLQENNIQTI~~  
SRAALAQLLKLEELHLD~~DNSISTVGVEDGAFREAI~~SLKLLFLSK~~NHLSSVPVGLPVDLQELR~~  
VDENRIAVISDMAFQNL~~TSLERLIVDG~~NLLTNKGIAEGTFS~~HLT~~KLKEFSIVRNSLSH~~PPP~~D  
LPGTHLIRYLQDNQINHIPLTA~~FSNL~~RKLERLDISNNQLRMLTQGVFDNL~~SNL~~KQLTARNN  
PWFCD~~CSIKWVTEWLKYIPSSLNVRGFMCQGPEQVRGM~~A~~VRELNM~~LLSCPTTPGLPLFTP  
APSTASPTTQP~~PTLSIPNPSRSY~~T~~PPPTTS~~KLPTIPDWDGRERVTPPI~~SERIQLSIHFVND~~  
TSIQVSWL~~SLFTVMAYKLTWVKM~~GHS~~LVGGIVQERIVSGEKQHLSLVN~~LEPRSTYRICLVPL  
DAFNYRAVEDTICSEATTHAS~~YLNNGSNTASSHEQTSHSMGSP~~FILLAGLIGGAVIFVLVVL  
LSVFCWHMHKKGRYTSQWKYNRGRR~~KDDYCEAGTKKD~~N~~SILEMTETSFQIVSLNNDQLLKG~~  
DFRLQPIYTPNGGINYTDCHI~~PNNMRYCNSSVPD~~LEHCHT

**Signal peptide:**

amino acids 1-42

**Transmembrane domain:**

amino acids 542-561

**N-glycosylation site.**

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

**Casein kinase II phosphorylation site.**

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

**Tyrosine kinase phosphorylation site.**

amino acids 319-328

**N-myristoylation site.**

amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,  
522-528, 545-551, 633-639

**Amidation site.**

amino acids 581-585

**Leucine zipper pattern.**

amino acids 164-186

**Phospholipase A2 aspartic acid active site.**

amino acids 39-50

## **FIGURE 14**

ACTTGGAGCAAGCGGCGGCCGGAGACAGAGGCAGAGGCAGAAGCTGGGGCTCCGTCTCGCCTCCCACGAGCG  
ATCCCCGAGGAGAGCCGCGGCCCTCGCGAGGCCAAGAGGCCACGAGGAAGACCCGGGTGGCTCGGCCCTGCC  
TCGCTTCCCAGGCAGGCCGGCTGCAGCCTTGCCCTCTTGCTCGCCTGAAATGGAAAAGATGCTCGCAGGCT  
GCTTCTGCTGATCCTCGGACAGATCGTCTCTCCCTGCGAGGCCAGGGAGCGTCAGTGAGGTTCCATCT  
CTAGGGCAGACACGCTCGGACCCACCGCAGACGGCCCTCTGGAGAGTTCTGAGAACAAGCAGGGAGACC  
TGGTTTCATCATTGACAGCTCTCGCAGTGTCAACACCCATGACTATGCAAAGGTCAAGGAGTTCATCGTGGACA  
TCTTGCATATTCTGGACATTGGCTCTGATGTCAACCCGAGTGGCCCTGCTCCAATATGGCAGCAGTGTCAAGAATG  
AGTTCTCCCTCAAGACCTTCAGAGGAAGTCCGAGGTGGAGCGTGTCAAGGAGATGCCGATCTGTCACGG  
GCACCATGACTGGCTGGGACATCCAGTATGCCCTGAAACATCGCATTCTCAGAACAGAGGGGCCGGCCCTGA  
GGGAGAATGTGCCACGGGCTATAATGATCGTCAAGATGGGAGACCTCAGGACTCCGTGGCCGAGGTGGCTGA  
AGGCACGGGACACGGGATCCTAATCTTGCATTGGTGGCCAGGTAGACCTTAACACCTTGAAGTCCATTG  
GGAGTGGAGCCCCATGAGGACCATGTCCTTGAGGAAATTTCAGCCAGATTGAGACGCTGACCTCCGTGTTCC  
AGAAGAAGTTGTGACGGGCCACATGTGAGCACCCCTGGAGCATAACTGTGCCACTTCTGCATCAACATCCCTG  
GCTCATACGTCAGGTGCAAACAGGCTACATTCTCAACTCGGATCAGACGACTTGAGAATCCAGGATCTGT  
GTGOCATGGAGGACCACACTGTGAGCAGCTGTGTGAATGTGCCGGCTCTCGTCTGCCAGTGCTACAGTG  
GCTACGCCCTGGCTGAGGATGGGAAGAGGTGTGGCTGGACTACTGTGCCCTCAGAAAACACGGATGTGAAC  
ATGAGTGTGTAATGCTGATGGCTCTACCTTGCCAGTGGCATGAAGGATTGCTCTTAACCCAGATGAAAAAA  
CGTGCACAAGGATCAACTACTGTGCACTGAACAAACCGGGCTGTGAGCATGAGTGCCTCAACATGGAGGAGGCT  
ACTACTGCCGCTGCCACCGTGGCTACACTCTGGACCCCAATGGCAAAACCTGCAAGCCGAGTGACCAACTGTGAC  
AGCAGGACCATGGCTGTGAGCAGCTGTGTGAACACGGAGGATTCCCTGCTGCCAGTGCTCAGAAGGCTCC  
TCATCAACGAGGACCTCAAGACCTGCTCCGGTGGATTACTGCCCTGCTGAGTGACCATGGTGTGAATACTCCT  
GTGTCACATGGACAGATCTTGCCCTGCTAGTGCTCTGAGGGACACGTGCTCCGAGCGATGGGAAGACGTGTG  
CAAATGGACTCTTGCTCTGGGACACGGTGTGAACATTGCTGTGAAGCAGTGAAAGATTGTTGTGT  
GCCAGTGTGTTGAAGGTTATATACTCCGTGAAGATGGAAAACCTGCAAGGAAAGATGTCGCAAGCTATAG  
ACCATGGCTGTGAACACATTGCTGAAACAGTGACGACTCATACACGTCGAGTGCTTGGAGGGATTCCGGCTCG  
CTGAGGATGGGAAACGCTGGCGAAGGAAGGATGTCTGCAAATCAACCCACCATGGCTGCAACACATTGTT  
ATAATGGGAAATTCTACATCTGCAAATGCTCAGAGGATTGTTCTAGCTGAGGACGGAAGACGGTGAAGAAAT  
GCACTGAAGGCCAATTGACCTGGTCTTGCTGATGGATCCAAGAGTCTTGGAGAAGAGAAATTGAGGTG  
TGAAGCAGTTGTCACTGGAATTATAGATTCTGACAATTCCCTAAAGCCGCTGAGTGGGCTGCTCCAGT  
ATTCCACACAGGTCCACACAGAGTTCACTCTGAGAAACTTCAACTCAGCCAAAGACATGAAAAAAAGCCGTGGCC  
ACATGAAATACTGGGAAAGGCTATGACTGGGCTGCCCTGAAACACATGTTGAGAGAAGTTTACCCAAG  
GAGAAGGGGCCAGGCCCTTCCACAAGGTGCCAGACCGAGCCATTGTTGACCGACGGACGGGCTCAGGATG  
ACGTCCTGGAGTGGCCAGTAAGGCAAGGCCAATGGTATCACTATGATGCTGTGGGCTAGGAAAGGCCATTG  
AGGAGGAACATACAAGAGATTGCCCTGAGGCCACAAACAAGCATCTTCTATGCCAGACTCAGCACAATGG  
ATGAGATAAGTAAAAACTCAAGAAAGGCATCTGTAAGCTCTAGAAGACTCGATGGAAGACAGGACTCTCCAG  
CAGGGGAACCTGCCAAAAACGGTCAACAGCCAACAGAATCTGAGCCAGTCACCATAAATATCCAAGACCTACTTT  
CCTGTTCTAATTGCACTGGCAGTGCACACAGATATCTGTTGAGAAGACAATCTTACGGCTACACAAAGCTTT  
CCCATTCAACAAACCTTCAGGAAGGCCCTTGGAAGAAAACAGATCAATGCAAATGTGAAACACCTTATAATGT  
TCCAGAACCTGCAACAGAAGTAAGAAAATTACACAGCGCTTAGAAGGAAATGACACAGAGAATGGAAGGCC  
TGGAAAATGCCCTGAGATAAGGATTAAGAATGCCACACATTGCTAGTCATTGCTACGGATTACAAT  
GAACGCAGTGCAGAGGCCAAAGCTCAGGCTATTGTTAAATCAATAATGTTGAGTAAACAAATCAGTACTGA  
GAAACCTGGTTGCCACAGAACAAAGACAAGAAGTATACTACACTAAGCTATGCAAGGTATTGTAATATACTGTGGACAC  
AACTGCTTCTGCCCTCATCCTGCCCTAGTGTGCAATCTCATTGACTATACGATAAAAGTTGCACAGTCTTACTT  
CTGTAGAACACTGCCATAGGAAATGCTGTTTTGACTTGGACTTACCTTGATATGTATATGGATGTATG  
CATAAAATCATAGGACATATGTAATTGAGGATTTTATACAATATAAAATTCAACACTTCAG

## **FIGURE 15**

MEKMLAGCFLLILGQIVLLPAEARERSGRSISRGRHARTHPOQTALLESSCENKRADLVFII  
DSSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGLLQYGSTVKNEFSLKTFKRKSEVERAV  
KMRHLSTGTMGLAIQYALNIAFSEAE GARPLRENVPRVIMIVTDGRPQDSVAEVAAKARD  
TGILIIFAIGVGQVDFTNLKSIGSEPHEDHVFLVANFSQIETLTSVFQKKLCTAHMCSTLEHN  
CAHFCINIPGSYVCRKQGYILNSDQTTCRIQDLCAMEDHNCEQLCVNPVPGSFVCQCYSGYA  
LAEDGKRCVAVDYCASENHGCEHECVNADGSYLCQCHEGFALNPDEKTCTRINYCALNKGPC  
EHECVNMEESYYCRCHRGYTLDPNGKTCRSVDHCAQQDHGEQLCLNTEDSFVCQCSEGFLI  
NEDLKTCSRVDYCLLSDHGCEYSCVNMDRSFACQCPEGHVLRS DGKTCAKLDSCALGDHGCE  
HSCVSSEDSFVCQCFCFGYILREDGKTCRRKDVCQAIDHGCEHICVNSDDSYTCECLEGFR LA  
EDGKRCRRKDVKSTHHGCEHICVNNNGNSYICKCSEG FVLAEDGRRCKCTEGPIDLVFVID  
GSKSLGEENFEVVKQFVTGIIDS LTISPKAARVGLLQYSTQVHTEFTLRNFMSAKDMKKAVA  
HMKYMGKGSMTGLALKHM FERSFTQGEGARPLSTRVPRAAIVFTDGRAQDDVSEWASKAKAN  
GITMYAVGVGKAIEELQEIA SEPTNKHLFYAEDFSTMDEISEKLKKGICEALEDSDGRQDS  
PAGELPKTVQQPT ESEPVTINI QDLLSCSNFAVQHRYLFEE DNLLRSTQKL SHSTKPSGSPL  
EEKHDQCKCENLIMFQNL ANEEVRKLTQRLEEMTQRMEALENRLRYR

**Signal peptide:**

amino acids 1-23

**N-glycosylation site.**

amino acids 221-225

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 115-119, 606-610, 892-896

**Casein kinase II phosphorylation site.**

amino acids 49-53, 118-122, 149-153, 176-180, 223-227, 243-247,  
401-405, 442-446, 501-505, 624-628, 673-677, 706-710, 780-784,  
781-785, 819-823, 866-870

**N-myristoylation site.**

amino acids 133-139, 258-264, 299-305, 340-346, 453-459, 494-500,  
639-645, 690-696, 752-758, 792-798

**Amidation site.**

amino acids 314-318, 560-564, 601-605

**Aspartic acid and asparagine hydroxylation site.**

amino acids 253-265, 294-306, 335-347, 376-388, 417-423, 458-464,  
540-546, 581-587

## **FIGURE 16**

GGAGCCGCCCTGGGTGTCAGCGCTCGCTCCCGCGCACGCTCCGCCGCGCAGCCTCG  
GCACCTGCAGGTCCGTGCGTCCCGCGCTGGCGCCCTGACTCCGTCCCGGCCAGGGAGGGC  
**CATGATTCCCTCCCCGGGCCCTGGTGACCAACTTGCTGCCGTTTGTTCTGGGCTGA**  
GTGCCCTCGCGCCCCCTCGCGGCCAGCTGCAACTGCACCTGCCGCCAACCGGTGCAAG  
GCGGTGGAGGGAGGGAAAGTGGTGTCCAGCGTGGTACACCTGCACGGGAGGGTGTCTTC  
ATCCCAGCCATGGGAGGTGCCCTTGATGTGGTCTTCAAACAGAAAGAAAAGGAGGATC  
AGGTGTTGTCTACATCAATGGGTACAACAAGCAAACCTGGAGTATCCTGGTCTACTCC  
ATGCCCTCCCGAACCTGTCCCTGCCGCTGGAGGGTCTCCAGGAGAAAGACTCTGGCCCCTA  
CAGCTGCTCCGTGAATGTGCAAGACAAACAAGGAAATCTAGGGCCACAGCATAAAACCT  
TAGAACTCAATGTACTGGTCTCCAGCTCCTCATCCTGCCGTCTCAGGGTGTGCCCAT  
GTGGGGCAAACGTGACCTGAGCTGCCAGTCTCCAAGGAGTAAGCCGCTGTCCAATACCA  
GTGGGATCGGCAGCTCCATCCTCCAGACTTCTTGACCAGCATTAGATGTCATCCGTG  
GGTCTTAAGCCTCACCAACCTTCGTCTTCCATGGCTGGAGTCTATGTCTGCAAGGCCAC  
AATGAGGTGGCACTGCCAATGTAATGTGACGCTGGAAGTGAGCACAGGCCCTGGAGCTGC  
AGTGGTTGCTGGAGCTGTTGGTACCCCTGGTGGACTGGGTTGCTGGCTGGCTGGTCC  
TCTTGTACCACCGCCGGCAAGGCCCTGGAGGAGCCAGCCAATGATATCAAGGAGGATGCC  
ATTGCTCCCCGGACCCTGCCCTGGCCCAAGAGCTCAGACACAATCTCAAGAATGGGACCC  
TTCCTCTGTCACCTCCGCACGAGCCCTCCGCCACCCATGGCCCTCCCAGGCCCTGGTCAT  
TGACCCCCACGCCAGTCTCTCCAGCCAGGCCCTGCCCTCACCAAGACTGCCACGACAGAT  
GGGCCCAACCTCAACCAATATCCCCCATCCCTGGTGGGTTCTCCTCTGGCTTGAGCCG  
CATGGGTGCTGTGCCTGTGATGGTGCCCTGCCAGAGTCAAGCTGGCTCTGGT**TATGATGAC**  
CCCACCACTATTGGCTAAAGGATTGGGCTCTCCTCTATAAGGGTACCTCTAGCAC  
AGAGGCCTGAGTCATGGAAAGAGTCACACTCCTGACCCCTAGTACTCTGCCCAACCTCTC  
TTTACTGTGGAAAACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGA  
AGTGGATCTGGAATTGGGAGGAGCCTCACCCACCCCTGACTCCTCTTATGAAGCCAGCTG  
CTGAAATTAGCTACTCACCAAGAGTGAGGGCAGAGACTTCCAGTCAGTCACTGAGTCTCCAGGC  
CCCCCTGATCTGATCCCCACCCCTATCTAACACCAACCCCTGGCTCCACTCCAGCTCCCTGT  
ATTGATATAACCTGTCAGGCTGGCTGGTTAGGTTTACTGGGAGGATAGGAAATCTC  
TTATTAACATGAAATATGTGTTTTCAATTGCAAATTAAATAAGATAACATAA  
TGTTGTATGAAAAA

## **FIGURE 17**

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEVSS  
SQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKDGPY  
SCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSKP  
AVQYQWDRQLPSFQTFFAPALD VIRGSLSLTNLSSSMAGVYVCKAHNEVGT  
AQCNVTLEVSTGPGAAVVAGAVVGTILVGLGLLAGLVLLYHRRGKALEEP  
PANDIKEDAIA PRTL PWPKSSDTISKNGTLSSVTSARALRPPHGPPRPGALTPTPSLSS  
SQALPS PRLPTTDGAHPQPISPIPGGVSSSGLSRMGAVPVMVPAQS  
QAGSLV

**Signal peptide:**

amino acids 1-29

**Transmembrane domain:**

amino acids 245-267

**N-glycosylation site.**

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

**N-myristoylation site.**

amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262,  
262-268, 308-314, 363-369, 364-370

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 164-175

## **FIGURE 18**

CGCCACCCTGCGGCCACCGCCA**AT**GAAACGCCTCCGCTCTAGGGTTTTCCACTTGTGAATTGTCCTATACTCAAAATTGACCAAGACACCTGTCTCCAAATGCAAAATGTGAATACGCAATGGAATTGAAGCCTGCTATTGCAACATGGGATTTCAGGAAATGGTGTACAAATTTGTGAAGATGATAATGAATGTGGAAATTAACTCAGTCTGTGGCGAAAATGCTAATTGCACTAACACAGAAGGAAGTTATTATTGTATGTGTACCTGGCTTCAGATCCAGCAGTAACCAAGACAGGTTTACTAATGATGGAACCGTCTGTATAGAAAATGTGAATGCAAATGCCCCATTAGATAATGTCTGTATAGCTGCAAATATTAACTTAACAAAAATCAGATCCATAAAAAGAACCTGTGGCTTGCTACAAGAAGTCTATAGAAATTCTGTGACAGATCTTCACCAACAGATATAATTACATATAGAAATATTAGCTGAATCATCTTCAACTTAGGTACAGAACAAACACTATCTCAGCCAAGGACACCCTTCTAACTCAACTCTTACTGAATTGTAACAAACCGTGAATAATTGTCAAAGGGATACATTGTAGTGTGGACAAGTTATCTGTGAATCATAGGAGAACACATCTTACAAAACATGCACACTGTGAACAAAGCTACTTTAAGGATATCCCAGAGCTTCCAAAAGACCACAGAGTTGATACAAATTCAACGGATATAGCTCTCAAAGTTTCTTTGATTCATATAACATGAAACATATTCTCCTCATATGAATATGGATGGAGACTACATAAAATATAATTCCAAAGAGAAAAGCTGCATATGATTCAAATGGCAATGTTGCAGTTGCATTTTATATTAGAGTATTGGCTCTTGCTTCATCATCTGACAACCTTCTATTGAAACCTCAAACATTATGATAATTCTGAAGAGGAGGAAAGAGTCATATCTCAGTAATTCTCAGTCTCAATGAGCTCAAACCCACCCACATTATGAACCTTACATTACATTAAGTCATCGAAAGGTACAGATAGGTATAGGAGTCTATGTGCATTGGAAATTACTCACCTGATACCATGAATGGCAGCTGGCTTCAGAGGGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGTGTAATCACCTGACACATTGTCAATTGTGATGTCCTCTGGCTTCCATTGGTATTAAAGATTATAATATTCTTACAAGGATCACTCAAATAGGAATAATTATTCACTGATTGTCTGCCATATGCATTTCACCTTCTGGTCTTCAGTGAACATTCAAAGCACCAGGACAACAATTCAAACAAATTCTTGTGCTAGCCTATTCTTCTGCTGAACCTGTTTTCTTGTGGATCAATACAAACTAATAAGCTCTCTGTTCAATCATTGCCGACTGCTACACTACTTCTTTAGCTGCTTTGCATGGATGTGCATTGAAGGCATACATCTTATCTCATTGTTGTGGGTGTCACTACAACAAAGGGATTGGCAAAAGAATTTTATATCTTGGCTATCTAACGCCCAGCGTGGTAGTGGATTTCGGCAGCACTAGGATACAGATATTATGGCACAAACAAAGTATGTTGGCTTAGCACCAGAAAACAACCTTATTGGAGTTTATAGGACAGCATGCCATTCTGTTAATCTCTTGGCTTTGGAGTCATCATACAAAGTTTCTCGTCACACTGCAGGGTTGAAACCAGAAGTTAGTTGCTTGGAGAACATAAGGTCTTGTGCAAGAGGAGCCCTCGCTCTGTTCTCGGCACCACCTGGATCTTGGGTCTCCATGTTGTGCAGCATTGAGCTTACAGCTTACAGCTTACACTTCTTCAACAGTCAGCAATGCTTCCAGGGATGTTCAATTCTTATTCTGTGTTTATCTAGAAAGATTCAAGAAGAATTACAGATTGTTCAAAATGTCCTGTTGTTGGATGTTAAGGTAACATAGAGAATGTTGGATAATTACAACACTGCACAAAATAAAATTCAAAGCTGTGGATGACCAATGTATAAAATGTTGACTCATCAAATTATCCAATTAACTACTAGACAAAAGTATTAAATCAGTTTCTGTTATGCTATAGGAACCTGTAGATAATAAGGTAACATTATGTATCATATAGATAACTATGTTTCTATGAAATAGTTCTGTCAAAATAGTATTGCAAGATATTGAAAGTAATTGGTTCTCAGGAGTGTATCACTGCACCAAGGAAAGATTCTTCTAACACGAGAAGTATGAACTGTCCTGAAGGAAACCACTGGCTTGATATTCTGTGACTCGTGTGGCCTTGAAACTAGTCCCTTACCCCTCGTAATGAGCTCATTACAGAAAGTGGAACATAAGAGAATGAAGGGCAGAATATCAAACAGTAAAAGGAATGATAAGATGTTTTGAATGAACTGTTTCTGTAGACTAGCTGAGAAATTGTTGACATAAAAATAAAAGAATTGAAAGAAACACATTACCTTACCTGGAA

## **FIGURE 19**

MKRLPLLVVFSTLLNCSYTQNCTKTPCLPNAKCEIRNGIEACYCNMGFSGNGVTICEDDNEC  
GNLTQSCGENANCTNTEGSYYCMCVPGRSSSNQDRFITNDGTVCIENVANCHLDNVCIAA  
NINKTLTKIRSIKEPVALLQEVRNSVTDLSPTDIITYIEILAESSLLGYKNNTISAKDTL  
SNSTLTFVKTVNNFVQRDTVVWDKLSVNHRRTHTKLMHTVEQATLRISQSFQKTTEFDT  
NSTDIALKFFFDSYNMKHIHPHMNMDGYINIFPKRKAAYDSNGNVAVAFLYYKSIGPLLS  
SSDNFLLPQNYDNSEEERVISSVISVSMSSNPPTLYELEKITFTLSRKVTDRYRSLCAF  
WNYSPDTMNGWSSEGCELTYSNETHTSCRNCNLTHFAILMSSGPSIGIKDYNILTRITQLG  
IIISLICLAICIFTWFFSEIQSTRTTIHKNLCCSLFLAELVFLVGINTNTNKLFCIIAGL  
LHYFFLAAFAWMCIEGIHLYLIVGVIVNKGLHKNFYIFGYLSPA VVGFSAALGYRYYGT  
TKVCWLSTENNFIWSFIGPACLIILVNLLAFGVIIYKVFRHTAGLKPEVSCFENIRSCARGA  
LALLFLLGTTWIFGVHLVVHASVVTAYLFTVSNAFQGMFIFLFLCVLSRKIQEEYYRLFKNV  
PCCFGCLR

**Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 430-450, 465-486, 499-513, 535-549, 573-593, 619-636,  
648-664

**N-glycosylation site.**

amino acids 15-19, 21-25, 64-68, 74-78, 127-131, 177-181,  
188-192, 249-253, 381-385, 395-399

**Glycosaminoglycan attachment site.**

amino acids 49-53

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 360-364

**Casein kinase II phosphorylation site.**

amino acids 54-58, 68-72, 76-80, 94-98, 135-139, 150-154,  
155-159, 161-165, 181-185, 190-194, 244-248, 310-314, 325-329,  
346-350, 608-612

**Tyrosine kinase phosphorylation site.**

amino acids 36-44, 669-677, 670-678

**N-myristoylation site.**

amino acids 38-44, 50-56, 52-58, 80-86, 382-388, 388-394,  
434-440, 480-486, 521-527

**Aspartic acid and asparagine hydroxylation site.**

amino acids 75-87

## **FIGURE 20**

TGGAAACATATCCTCCCTCATATGAATATGGATGGAGACTACATAAATATATTCCAAAGNG  
AAAAGCCGGCATATGGATTCAAATGGCAATGTTGCAGTTGCATTTTATATTATAAGAGTAT  
TGGTCCCTTGCTTCATCATCTGACAACCTCTTATTGAAACCTCAAAATTATGATAATTCT  
GAAGAGGAGGAAAGAGTCATATCTTCAGTAATTCACTGAGCTCAAACCCACCCAC  
ATTATATGAACTTGAAAAAACATTACATTAAGTCATCGAAAGGTACAGATAGGTATA  
GGAGTCTATGTGGCATTGGAAACTCACCTGATACCATGAATGGCAGCTGGTCTTCAGAG  
GGCTGTGAGCTGACACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCTGACACA  
TTTGCAATTGATGTCCTCTGGCCTTCCATTGGTATTAAAGATTATAATATTCTTACAA  
GGATCACTCAACTAGGAATAATTATTCACTGATTGTCTGCCATATGCATTTACCTTC  
TGGTTCTTCAGTGAAATTCAAAGCACCAGGA

## **FIGURE 21**

GCTCCCAGCCAAGAACCTGGGGCCGCTGCGCGGTGGGGAGGAGTCCCCGAAACCCGGCCG  
CTAAGCGAGGCCTCCTCCTCCCGCAGATCCGAACGGCCTGGCGGGGTCAACCCGGCTGGGA  
CAAGAACGCCCGCCTGCCTGCCCGGGGCCGGAGGGGGCTGGGCTGGGCCGGAGGCGG  
GGTGTGAGTGGGTGTGCGGGGGGGCGAGGCTTGATGCAATCCCATAAGAAATGCTCGGG  
TGTCTGGCACCTACCCGTGGGGCCCGTAAGGCGCTACTATATAAGGCTGCCGGCCGGAG  
CCGCCGCGCCGTAGAGCAGGAGCGCTCGTCCAGGATCTAGGCCACGACCATCCAAACCC  
GGCACTCACAGCCCCAGCGCATCCGGTCGCCGCCAGCCTCCGCACCCCCATGCCGG  
AGCTGCGCCGAGAGCCCCAGGGAGGTGCCATGCGGAGCGGGTGTGTTGGTCCACGTATGG  
ATCCTGGCCGGCCTCTGGCTGGCGTGGCCGGCGCCCCCTCGCCTTCTCGGACGCGGGGCC  
CCACGTGCACTACGGCTGGGCGACCCCATCCGCCTGCGCACCTGTACACCTCCGGCCCCC  
ACGGGCTCTCCAGCTGCTTCCGCATCCGTGCCGACGGCGTGGACTGCGCGGGGGC  
CAGAGCGCGCACAGTTGCTGGAGATCAAGGCAGTCGCTCTGCGGACCGTGGCCATCAAGGG  
CGTGCACAGCGTGCCTGACCTCTGCATGGCGCCGACGGCAAGATGCAGGGCTGCTTCAGT  
ACTCGGAGGAAGACTGTGCTTCGAGGAGGAGATCCGCCAGATGGCTACAATGTGTACCGA  
TCCGAGAAGCACGCCCTCCGGTCTCCCTGAGCAGTGCAAACAGCGGAGCTGTACAAGAA  
CAGAGGCTTCTTCCACTCTCTCATTCCGCATGCTGCCCATGGTCCAGAGGAGCCTG  
AGGACCTCAGGGGCCACTTGGAAATCTGACATGTTCTTCGCCCTGGAGACCGACAGCATG  
GACCCATTGGGCTTGTCAACGGACTGGAGGGCGTGAGGAGTCCAGCTTGAGAAGTAACT  
GAGACCATGCCCGGGCCTCTCACTGCTGCCAGGGCTGTGGTACCTGCAGCGTGGGAGC  
TGCTTCTACAAGAACAGTCCTGAGTCCACGTTCTGTTAGCTTAGGAAGAACATCTAGAA  
GTTGTACATATTCAAGAGTTTCCATTGGCAGTGCAGTTCTAGCCAATAGACTTGTCTGAT  
CATACATTGTAAGCCTGTAGCTGCCAGCTGCTGCCCTGGCCCCATTCTGCTCCCTCGA  
GGTTGCTGGACAAGCTGCTGCACTGTCAGTTCTGCTGAATACCTCCATCGATGGGAAC  
TCACTTCCTTGGAAAAATTCTTATGTCAAGCTGAAATTCTCTAATTTCATCACTTC  
CCCAGGAGCAGCCAGAACAGACAGGAGTAGTTAATTCAAGAACAGGTGATCCACTCTGTA  
AAACAGCAGGTAATTCACTCAACCCATGTGGAATTGATCTATCTACTTCCAGGG  
ACCATTGCCCTCCCAAATCCCTCCAGGCCAGAACCTGACTGGAGCAGGCATGGCCCACCGAG  
GCTTCAGGAGTAGGGGAAGCCTGGAGCCCCACTCCAGCCCTGGGACAACTTGAGAATTCCCC  
CTGAGGCCAGTTCTGTCATGGATGCTGCTGAGAATAACTTGCTGTCCCGGTGTCACCTGC  
TTCCATCTCCAGGCCACCAGCCCTCTGCCACCTCACATGCCTCCCATGGATTGGGCCT  
CCCAGGCCCCCACCTTATGTCAACCTGCACCTCTGTTCAAAAATCAGGAAAAGAAAAGAT  
TTGAAGACCCCAAGTCTGTCAATAACTTGCTGTGGAAGCAGGGGGAGACCTAGAAC  
CCTTCCCCAGCACTGGTTTCCAACATGATATTATGAGTAATTATTTGATATGTACA  
TCTCTTATTTCTTACATTATTATGCCCAAATTATATTATGTATGTAAGTGAGGTTG  
TTTGTATATTAAAATGGAGTTGTTGT

## **FIGURE 22**

MRSGCVVVHVWILAGLWLAVAGRPLAFSDAGPHVHYGWDPIRLRHLYTSGPHGLSSCFLRI  
RADGVVDCARGQSAHSLLEIKAVALRTVAIKGVHSVRYLCMGADGKMQGLLQYSEEDCAFEE  
EIRPDGYNVYRSEKHLPLVSSLSSAKQRQLYKNRGFLPLSHFLPMLPMVPEEPEDLRGHLESD  
MFSSPLETDSMDPFGLVTGLEAVRSPSFEK

**Signal peptide:**

amino acids 1-22

**Casein kinase II phosphorylation site.**

amino acids 78-82, 116-120, 190-194, 204-208

**N-myristoylation site.**

amino acids 15-21, 54-60, 66-72, 201-207

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 48-59

## **FIGURE 23**

CCCAGAACGTTCAAGGGCCCCCGGCCTCCTGCGCTCCTGCCGCCGGGACCCCTGACCTCCTCA  
GAGCAGCCGGCTGCCGCCGGGAAGATGGCGAGGAGGAGCCACCGCCTCCTGCTG  
CTGCTGCGCTACCTGGTGGTCGCCCTGGGCTATCATAAGGCCTATGGGTTTCTGCCAAA  
AGACCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGCTATTTAGCCTGCAAACCCCAA  
AGAAGACTGTTCCAGATTAGAGTGGAAAGAACTGGGTGGAGTGTCTCCTTGCTAC  
TATCAACAGACTCTCAAGGTGATTTAAAAATCGAGCTGAGATGATAGATTTCAATATCCG  
GATCAAAATGTGACAAGAAGTGATGCCGGAAATATCGTTGTGAAGTTAGTGCCTCATCTG  
AGCAAGGCCAAACCTGGAAGAGGATAACAGTCACACTGGAAGTATTAGTGGCTCCAGCAGTT  
CCATCATGTGAAGTACCCCTTCTGCTCTGAGTGGAACTGTGGTAGAGCTACGATGTCAAGA  
CAAAGAAGGAAATCCAGCTCCTGAATACACATGGTTAAGGATGGCATCCGTTGCTAGAAA  
ATCCCAGACTGGCTCCAAAGCACCAACAGCTCATACACAATGAATACAAAAACTGGAAC  
CTGCAATTAAACTGTTCCAAACTGGACACTGGAGAATATTCCGTGAAGCCGCAATT  
TGTTGGATATCGCAGGTGTCCTGGAAACGAATGCAAGTAGATGATCTAACATAAGTGGCA  
TCATAGCAGCCGTAGTAGTTGTGGCCTTAGTGATTCCGTTGTGGCCTGGTGTATGCTAT  
GCTCAGAGGAAAGGCTACTTCAAAAGAAACCTCCTCCAGAAGAGTAATTCTCATCTAA  
AGCCACGACAATGAGTGAATGTGCAGTGGCTACGCCTGTAATCCCAGCACTTGGAAAGG  
CCGGCGGGCGGATCACGAGGTCAGGAGTTCTAGACCAGTCTGGCAATATGGTAAACCC  
CATCTCTACTAAAATACAAAAATTAGCTGGCATGGTGGCATGTGCCCTGCAGTTCCAGCTGC  
TTGGGAGACAGGAGAACACTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCTGAGATCACGC  
CACTGCAGTCCAGCCTGGTAACAGAGCAAGATTCCATCTCAAAAAATAAATAAATA  
AATAAATACTGGTTTACCTGTAGAATTCTTACAATAATAGCTTGATATT

## **FIGURE 24**

MARRSRHRLLLLLRYLVVALGYHKAYGFSAPKQQVVTAVEYQEAILACKTPKKTVSSRLE  
WKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEED  
TVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKD GIRLLENPRILGSQST  
NSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNISGIIAAVVVA  
LVISVCGLGV CYAQRKGYFSKETSFQKSNSSSKATTMSENVQWLTPVIPALWKA AAGGSRGQEF

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 130-144, 238-258

**N-glycosylation site.**

amino acids 98-102, 187-191, 236-240, 277-281

**Casein kinase II phosphorylation site.**

amino acids 39-43, 59-63, 100-104, 149-153, 205-209, 284-288

**N-myristoylation site.**

amino acids 182-188, 239-245, 255-261, 257-263, 305-311

**Amidation site.**

amino acids 226-230

## **FIGURE 25**

GACATCGGAGGTGGCTAGCACTGAACTGCTTTCAAGACGAGGAAGAGGAGGAGAAAGAG  
AAAGAAGAGGAAGATGTTGGCAACATTATTTAACATGCTCCACAGCCCGGACCTGGCAT  
CATGCTGCTATTCTGCAAATACTGAAGAAGCATGGATTAAATATTTACTTCTAAATAA  
ATGAATTACTCAATCTCCTATGACCACACTACATACACTCCACCTCAAAAAGTACATCAATA  
TTATATCATTAAAGGAAATAGTAACCTCTTCTCCAATATGCATGACATTGGACAATG  
CAATTGTGGCACTGGCACTTATTTCAGTGAAGAAAAACTTGTGGTTATGGCATTCA  
TTTGACAAATGCAAGCATCTCCTTATCAATCAGCTCTATTGAACTTACTAGCACTGACTG  
TGGAATCCTTAAGGGCCATTACATTCTGAAGAAGAAAGCTAAGATGAAGGACATGCCACT  
CCGAATTCACTGTGCTACTTGGCCTAGCTATCACTACACTAGTACAAGCTGTAGATAAAAAAG  
TGGATTGTCCACGGTTATGTACGTGTGAAATCAGGCCTGGTTACACCCAGATCCATTAT  
ATGGAAGCCTACAGTGGATTGTAATGATTAGGTCTTTAACCTTCCCAGCCAGATTGCC  
AGCTAACACACAGATTCTCTCACAGACTAACAAATATTGAAATACTCCACAG  
ACTTTCCAGTAAACCTACTGGCCTGGATTATCTCAAAACAATTATCTCAGTCACCAAT  
ATTAATGTAAGGAAAGATGCCTCAGCTCCTTCTGTGTACCTAGAGGAAACAAACTACTGA  
ACTGCCTGAAAATGTCTGCGAACTGAGCAACTACAAGAACTCTATATTAACTACAACT  
TGCTTCTACAATTTCACCTGGAGCCTTATTGGCCTACATAATCTCTTCGACTTCATCTC  
AATTCAAATAGATTGCAGATGATCAACAGTAAGTGGTTGATGCTCTCCAAATCTAGAGAT  
TCTGATGATTGGGAAATCCAATTATCAGAACATCAAAGACATGAACTTTAACCTCTTATCA  
ATCTTCGAGCCTGGTTATAGCTGGTATAAACCTCACAGAAATACAGATAACGCCTGGTT  
GGACTGGAAAACCTAGAAAGCATCTCTTTACGATAACAGGCTTATTAAAGTACCCCATGT  
TGCTCTCAAAAGTTGTAATCTCAAATTGGATCTAAATAAAACCTATTAAAGA  
TACGAAGGGGTGATTAGCAATATGCTACACTAAAAGAGTTGGGATAAATAATATGCCT  
GAGCTGATTCCATCGATAGTCTGCTGTGGATAACCTGCCAGATTAAAGAAAATAGAAGC  
TACTAACACCCCTAGATTGTCTTACATTCAACCCCAATGCATTTCAGACTCCCCAAGCTGG  
AATCACTCATGCTGAACAGCAATGCTCAGTGCCCTGTACCATGGTACCATGGTACCATGAGTCTCTG  
CCAAACCTCAAGGAAATCAGCATACACAGTAACCCATCAGGTGTGACTGTGTCATCCGTTG  
GATGAACATGAACAAAACCAACATTGATTGATGGAGCCAGATTCACTGTTGCGTGGACC  
CACCTGAATTCCAAGGTCAAGATGTTGGCAAGTGCATTTCAGGGACATGATGAAATTGT  
CTCCCTCTTATAGCTCCTGAGAGCTTCTTCTAAATCTAAATGTAGAAGCTGGAGCTATGT  
TTCCCTTCACTGTAGAGCTACTGCAGAACACAGCCTGAAATCTACTGGATAACACCTTCTG  
GTCAAAAACCTTGCCTAATACCCCTGACAGACAAGTTCTATGTCCATTCTGAGGGAAACACTA  
GATAAAATGGCGTAACTCCAAAGAAGGGGTTATATACTTGTATAGCAACTAACCTAGT  
TGGCGCTGACTTGAAGTCTGTTATGATCAAAGTGGATGGATCTTCCACAAAGATAACAAATG  
GCTCTTGAATATTAAAAGAGATATTCAAGGCCAATTCAAGTTGGTGTCTGGAAAGCA  
AGTTCTAAAATTCTCAAATCTAGTGTAAATGGACAGCCTTGTCAAGACTGAAATTCTCA  
TGCTGCGCAAAGTGCCTGAATACCATCTGATGTCAGGTATATAATCTTACTCATCTGAATC  
CATCAACTGAGTATAAAATTGTATTGATATTCCCACCATCTATCAGAAAACAGAAAAAAA  
TGTGTAATGTCACCACCAAGGTTGCACCCCTGATCAAAAGAGTATGAAAAGAATAATAC  
CACAAACACTTATGGCCTGTCTGGAGGCCTCTGGGATTATGGTGTGATATGTCTTATCA  
GCTGCCTCTCCAGAAATGAACTGATGGTGACACAGCTATGTGAGGAATTACTTACAG  
AAACCAACCTTGCATTAGGTGAGCTTATCCTCTGTATAATCTGGGAAGCAGGAAA  
AGAAAAAAAGTACATCACTGAAAGTAAAAGCAACTGTTAGGTTACCAACAAATATGTCCT  
AAAAACCAAGGAAACCTACTCCAAAATGAAC

## **FIGURE 26**

MKDMLPLRIHVLLGLAITTLVQAVDKVDCPRLCTCEIRPWFTPRSIYMEASTVDCNDLGLLT  
FPARLPANTQILLLQTNNIAKIEYSTDFPVNLTLGDLDSQNNLSSVTNINVKKMPQLLSVYLE  
ENKLTELPEKCLSELSNLQELYINHNLLSTISPGAFIGLHNLLRLHNSNRLOMINSKWFDA  
LPNLEILMIGENPIIIRIKDMNFKPLINLRSLVIAGINLTEIPDNALVGLENLESISFYDNRL  
IKVPHVALQKVNLKFDDLNKNPINRIRRQDFSNMLHLKELGINNMPELISIDS LAVDNLPD  
LRKIEATNNPRLSYIHPNNAFFRLPKLESMLNSNALSALYHGTIESLPNLKEISIHSNPIRC  
DCVIRWMNMNTNIRFMEPDSLFCVDPPEFQGQNVHQVFRDMMEICLPLIAPESFPSNLNV  
EAGSYVSFHCRATAEPQPEIYWITPSGQKLLPNTLTDKFYVHSEGTLINGVTPKEGGLYTC  
IATNLVGADLKSVMIKVDGSFPQDNNGSLNIKIRDIQANSVLVSKASSKILKSSVKWTAFV  
KTENSHAAQSARI PSDVKVYNLTHLN PSTEYKICIDIPTIYQKNRKKCVNVTTKGLHPDQKE  
YEKNNTTTLMACLGGLLGIIGVICLISCLSPEMNCDGGHSYVRNYLQKPTFALGELYPP LIN  
LWEAGKEKSTS LKV KATV IGLPTNMS

**Signal sequence:**

amino acids 1-22

**Transmembrane domain:**

amino acids 633-650

**N-glycosylation site.**

amino acids 93-97, 103-107, 223-227, 382-386, 522-526, 579-583,  
608-612, 624-628, 625-629

**Casein kinase II phosphorylation site.**

amino acids 51-55, 95-99, 242-246, 468-472, 487-491

**Tyrosine kinase phosphorylation site.**

amino acids 570-579

**N-myristoylation site.**

amino acids 13-19, 96-102, 158-164, 221-227, 352-358, 437-443,  
491-497, 492-498, 634-640, 702-708

**Cell attachment sequence.**

amino acids 277-280

## **FIGURE 27**

GCCCCGGACTGGCGCAAGGTGCCAAGCAAGGAAAGAAATAATGAAGAGACACATGTGTTAG  
CTGCAGCCTTTGAAACACGCAAGAAGGAAATCAATAGTGTGGACAGGGCTGGAACCTTAC  
CACGCTTGTGGAGTAGATGAGGAATGGGCTCGTGAATTATGCTGACATTCCAGCATGAATCT  
GGTAGACCTGTGGTTAACCGTTCCCTCTCATGTGTCTCCTACAAAGTTTGTTCTTA  
TGATACTGTGCTTCATTCTGCCAGTATGTGTCCAAGGGCTGTCTTGTCTCCTCTGGG  
GGTTAAATGTCACCTGTAGCAATGCAAATCTCAAGGAAATACCTAGAGATCTCCTCCTGA  
AACAGTCTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCAATGAAATTAAAGG  
ACCTCCATCAACTGAGAGTTCTAACCTGTCCAAAATGGCATTGAGTTATCGATGAGCAT  
GCCTCAAAGGAGTAGCTGAAACCTTGCAGACTCTGGACTTGTCCGACAATCGGATTCAAAG  
TGTGCACAAAATGCCTTCATAAACCTGAAGGCCAGGGCAGAATTGCCAACAAACCCCTGGC  
ACTGCGACTGTACTCTACAGCAAGTTCTGAGGAGCATGGCGTCAATCATGAGACAGCCCAC  
AACGTGATCTGTAAAACGTCCGTGTTGGATGAACATGCTGGCAGACCATTCTCAATGCTGC  
CAACGACGCTGACCTTGTAAACCTCCCTAAAAAAACTACCGATTATGCCATGCTGGTCACCA  
TGTTGGCTGGTCACTATGGTGAATCTCATATGTGGTATATTATGTGAGGCAAATCAGGAG  
GATGCCCGAGACACCTCGAATACTTGAAATCCCTGCCAAGCAGGAGAAGAAAGCAGATGA  
ACCTGATGATATTAGCACTGTGGTATAGTGTCCAAACTGACTGTCAATTGAGAAAGAAAGAAA  
GTAGTTGCGATTGCACTAGAAATAAGTGGTTACTTCTCCATCCATTGTAAACATTGAA  
ACTTGTATTTCAGTTTTGAAATTATGCCACTGCTGAACCTTAACAAACACTACAACA  
TAAATAATTGAGTTAGGTGATCCACCCCTTAATTGTACCCCCGATGGTATATTCTGAGT  
AAGCTACTATCTGAACATTAGTTAGATCCATCTCACTATTAAATAATGAAATTATTTTTT  
AATTAAAAGCAAATAAAAGCTTAACCTTGAACCAGGGAAAAAAAAAAAAAAACA

## **FIGURE 28**

MNLVDLWLTRSLSMCLLQSFVLMILCFHSASMC PKGCLSSSGGLNVTC SNANLKEIPRDL  
PPETVLLYLDNSNQITSIPNEIFKDLHQLRVLNLSKNGIEFIDEHAFKGVAETLQTLSDLSDNR  
IQSVHKNAFNNLKARARIANNPWHCDCTLQQVLRSMASN HETAHNVICKTSVLDEHAGR PFL  
NAANDADLCNLPKKTTDYAMLVTMFGWFTMVISYVVYYVRQNQEDARRHLEYLKSLPSRQKK  
ADEPDDISTVV

**Signal sequence:**

amino acids 1-33

**Transmembrane domain:**

amino acids 205-220

**N-glycosylation site.**

amino acids 47-51, 94-98

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 199-203

**Casein kinase II phosphorylation site.**

amino acids 162-166, 175-179

**N-myristoylation site.**

amino acids 37-43, 45-51, 110-116

## **FIGURE 29**

ACCGAGCCGAGCGAACGAAGGCAGCCCCGAGATGAGGTGAGCAAGAGGATGCTGGCGGG  
GGCGTGAGGAGCATGCCAGCCCCCTCTGGCCTGCTGGCAGCCCATTCTCTGCTGGTGCT  
GGGCTCAGTGTGTCAGGCTGGCCACGGCTGCCGCCGCTGCGAGTGCTCCGCCAGG  
ACCGCGCTGTGCTGTGCCACCGCAAGTGCTTGCGACTCCCCGAGGGCATCCCCACCGAG  
ACGCGCTGCTGGACCTAGGCAAGAACCGCATAAAACGCTCAACCAGGACGAGTTGCCAG  
CTTCCCGCACCTGGAGGAGCTGGAGCTCAACGAGAACATCGTAGGCGCTGGAGGCCGG  
CCTTCAACAAACCTCTCAACCTCCGGACGCTGGGTCTCCGAGCAACCGCCTGAAGCTCATC  
CCGCTAGGCGTCTTCACTGGCCTCAGAACCTGACCAAGCAGGACATCAGCGAGAACAGAT  
CGTTATCCTACTGGACTACATGTTCAGGACCTGTACAACCTCAAGTCAGTGAGGTTGGCG  
ACAATGACCTCGTCTACATCTCACCGCGCTCAGCGGCCTCAACAGCCTGGAGCAGCTG  
ACGCTGGAGAAATGCAACCTGACCTCCATCCCCACCGAGGGCGCTGCCCACCTGCACGGCCT  
CATCGTCTGAGGCTCGGCACCTCAACATCAATGCCATCCGGACTACTCCTTAAGAGGC  
TGTACCGACTCAAGGTCTGGAGATCTCCACTGGCCTACTTGGACACCATGACACCCAAC  
TGCCTCTACGGCCTCAACCTGACGTCCCTGTCCATCACACACTGCAATCTGACCGCTGTGCC  
CTACCTGGCGTCCGCCACCTAGTCTATCTCGCTTCCTCAACCTCTCCTACAACCCCCATCA  
GCACCATTGAGGGCTCCATGTTGATGAGCTGCTCCGGCTGCAGGAGATCCAGCTGGTGGCG  
GGGCAGCTGGCGTGGTGGAGGCCCTATGCCTTCCGGCCTCAACTACCTGCGCGTCTCAA  
TGTCTCTGGCAACCAGCTGACCAACTGGAGGAATCAGTCTTCACTCGTGGCAACCTGG  
AGACACTCATCCTGGACTCCAACCGCTGGCGACTGTCGGCTCCTGTGGGTGTTCCGG  
CGCCGCTGGCGCTCAACTTCAACCGGAGCAGGCCACGTGCGCACGCCAGTTGTC  
GGGCAAGGAGTTCAAGGACTTCCCTGATGTGCTACTGCCAACTACTTCACCTGCCCGCG  
CCCGCATCCGGGACCGCAAGGCCAGCAGGTGTTGTGGACGAGGCCACCGGTGAGTT  
GTGTGCCGGCGATGGCGACCGGCCCATCCTCTGGCTCTCACCCGAAAGCACCT  
GGTCTCAGCCAAGAGCAATGGCGGCTCACAGTCTTCCCTGATGGCACGCTGGAGGTGCGCT  
ACGCCCAAGGTACAGGACAACGGCACGTACCTGTGCATCGCGGCCAACGCCGGCAACGAC  
TCCATGCCGCCACCTGCATGTGCGCAGCTACTGCCACTGGCCCCATCAGCCCAACAA  
GACCTTCGCTTTCATCTCAACCAGCGGGCGAGGGAGAGGCCAACAGCACCCGCGCACTG  
TGCCTTCCCTTCGACATCAAGACCTCATCATGCCACCCATGGCTCATCTCTTTC  
CTGGCGTCGCTCTTCTGCCCTGGTGTGCTGTTCTGGAGGCCAGGGCAACAC  
AAAGCACAACATCGAGATCGAGTATGTCCCCGAAAGTCGGACGCAGGCATCAGCTCCGCG  
ACGCCCAAGGTCAACATGAAGATGATATGAGGCCGGGGCGGGGGCAGGGACCCCCG  
GGCGGCCGGCGAGGGGAAGGGGCCTGGTGCACCTGCTCACTCTCCAGTCCTCCACCTC  
CTCCCTACCCCTCTACACACGTTCTCTTCTCCCTCCGCCCTCCGCTCCCTGCTGCCCG  
CCAGCCCTCACCACCTGCCCTCTTCTACAGGACCTCAGAACGCCAGACCTGGGACCCCA  
CCTACACAGGGCATTGACAGACTGGAGTTGAAAGCCGACGAACCGACACGCCAGAGTC  
ATAATTCAATAAAAAAGTTACGAACCTTCTCTGTAACCTGGTTCAATAATTATGGATTT  
TATGAAAACCTGAAATAATAAAAAAGAGAAAAAAACTAAAAAAAAAAAAAA

## **FIGURE 30**

MQVSKRMLAGGVRSMPSPLLACWQPILLVLGSVLSGSATGCPPCECSAQDRAVLCHRKCF  
VAVPEGIPTETRLLDLGKNRIKTLNQDEFASFPHLEELENENIVSAVEPGAFNNLFNLRTL  
GLRSNRKLIPLGVFTGLSNLTKQDISENKIVILLDYMFQDLYNLKSLEVGDNDLVYISHRA  
FSGLNSLEQLTLEKCNLTSIPTEALSHLHGLIVLRLRHLNINAIRDYSFKRLYRLKVLEISH  
WPYLDTMTPNCLYGLNLTSLSITHCNLTAVPYLAVRHLVYLRFNLNSYNPISTIEGSMLHEL  
LRLQEIQLVGGQLAVVEPYAFRGLNYLRLVNVSGNQLTTLEESVFHSVGNLETLILDSNPLA  
CDCRLLWVFRRRWRLLNFNRQQPTCATPEFVQGKEFKDFPDVLLPNYFTCRRARIRDRKAQQV  
FVDEGHTVQFVCRADGDPPPAILWLSPRKHLVSAKSNGRLTVFPDGTLLEVRYAQVQDNGTYL  
CIAANAGGNDNSMPAHLHVRSYSPDWPHQPNKTFAFISNQPGEGEANSTRATVPFPFDIKTLI  
IATTMGFISFLGVVLFCVLFLWSRGKGNTKHNIEIEYVPRKSDAGISSADAPRKFNMKMI

**Signal sequence:**

amino acids 1-41

**Transmembrane domain:**

amino acids 556-578

**N-glycosylation site.**

amino acids 144-148, 202-206, 264-268, 274-278, 293-297, 341-345,  
492-496, 505-509, 526-530, 542-546

**Casein kinase II phosphorylation site.**

amino acids 49-53, 108-112, 146-150, 300-304, 348-352, 349-353,  
607-611

**Tyrosine kinase phosphorylation site.**

amino acids 590-598

**N-myristoylation site.**

amino acids 10-16, 32-38, 37-43, 113-119, 125-131, 137-143,  
262-268, 320-326, 344-350, 359-365, 493-499, 503-509, 605-611

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 32-43

## **FIGURE 31**

CCCACGCGTCCGCACCTCGGCCCGGGCTCCGAAGCGGCTCGGGGGGCCCTTCGGTCAAC  
ATCGTAGTCCACCCCTCCCCATCCCCAGCCCCGGGGATTCAAGGCTGCCAGCGCCCAGCC  
AGGGAGCCGGCGGGAAAGCGCG**A**TGGGGGCCAGCCGCTCGCTCCTGCTCCTGC  
TGTTCGCCTGCTGGCGCCGGCGGGCCAACCTCTCCAGGACGACAGCCAGCCCTGG  
ACATCTGATGAAACAGTGGTGGCTGGTGGCACCGTGGTCAAGTGCAAGTGAAAGATCA  
CGAGGACTCATCCCTGCAATGGTCAACCCTGCTCAGCAGACTCTACTTTGGGAGAAGA  
GAGCCCTTCGAGATAATCGAATTCAAGCTGGTACCTCTACGCCAACGAGCTCAGCATCAGC  
ATCAGCAATGTGGCCCTGGCAGACGAGGGCGAGTACACCTGCTCAATCTTCACTATGCCGTG  
GCGAACTGCCAAGTCCCTCGTCACTGTGCTAGGAATTCCACAGAACCCATCATCACTGGTT  
ATAAACTTCATTACGGGAAAAAGACACAGCCACCCCTAAACTGTCAGTCTCTGGGAGCAAG  
CCTGCAGCCGGCTCACCTGGAGAAAGGGTGACCAAGAACCTCACGGAGAACCAACCCGCAT  
ACAGGAAGATCCAATGGTAAAACCTTCACTGTCAGCAGCTGGTACATTCCAGGTTACCC  
GGGAGGATGATGGGCGAGCATCGTGTGCTCTGTGAACCATGAATCTCTAAAGGGAGCTGAC  
AGATCCACCTCTCAACGCATTGAAGTTTATACACACCAACTGCGATGATTAGGCCAGACCC  
TCCCCATCCTCGTGAGGGCAGAAGCTGTTGCTACACTGTGAGGGTCGGCAATCCAGTCC  
CCCAGCAGTACCTATGGGAGAAGGAGGGCAGTGTGCCACCCCTGAAGATGACCCAGGAGAGT  
GCCCTGATCTCCCTTCCTCAACAAGAGTGACAGTGGCACCTACGGCTGCACAGCCACCA  
AACATGGGCAGCTACAAGGCCTACTACACCCCTCAATGTTAATGACCCAGTCCGGTGCCT  
CCTCCTCCAGCACCTACCACGCCATCATCGTGGGATCGTGGCTTCATTGTCTCCTGCTG  
CTCATCATGCTCATCTTCCCTGGCCACTACTTGATCCGGCACAAAGGAACCTACGTGACACA  
TGAGGCAAAAGGCTCCGACGATGCTCCAGACGCGGACACGGCCATCATCAATGCAGAAGGCG  
GGCAGTCAGGAGGGGACGACAAGAAGGAATATTCA**T**AGAGGCGCTGCCACTTCCTGC  
GCCCCCAAGGGGCCCTGTGGGACTGCTGGGCCGTACCAACCCGGACTTGTACAGAGCAA  
CCGCAGGGCCGCCCTCCCGCTTGTCCCCAGCCCACCCACCCCTGTACAGAAATGTCTGC  
TTGGGTGCGGTTTGTACTCGGTTGGAATGGGGAGGGAGGAGGGCGGGGGAGGGAGGG  
TTGCCCTCAGCCCTTCCGTGGCTCTGCATTGGTTATTATTATTTGTAACAATCC  
CAAATCAAATCTGTCTCCAGGCTGGAGAGGCAGGAGGCCCTGGGTGAGAAAAGCAAAAACA  
AACAAAAAACAA

## **FIGURE 32**

MGAPAASLLLLLFFACCWAPGGANLSQDDSQWPWTSDETVVAGGTVVLCQVKDHEDSSLQW  
SNPAQQTLYFGEKRALRDNRSQLVTSTPHELSIISNVALADEGEYTCSIFTMPVRTAKSLV  
TVLGIPQKPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGQELHGEPTRIQEDPNGK  
TFTVSSSVTFQVTREDDGASIVCSVNHESLKGADRSTSQRIEVLYTPTAMIRPDPPHPREGQ  
KLLLHCEGRGNPVPQQYLWEKEGSVPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKA  
YYTLNVNDPSPVPSSSSTYHAIIGGIVAFIVFLLIMLIFLGHYLIRHKGTYLTHEAKGSDD  
APDADTAIINAEGGQSGGDDKKEYFI

**Signal sequence:**

amino acids 1-20

**Transmembrane domain:**

amino acids 331-352

**N-glycosylation site.**

amino acids 25-29, 290-294

**Casein kinase II phosphorylation site.**

amino acids 27-31, 35-39, 89-93, 141-145, 199-203, 388-392

**N-myristoylation site.**

amino acids 2-8, 23-29, 156-162, 218-224, 295-301, 298-304,  
306-310, 334-340, 360-364, 385-389, 386-390

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18

## **FIGURE 33**

GGGGGTTAGGGAGGAAGGAATCCACCCCCACCCCCCAAACCCCTTCTCTCCTTCCTGG  
CTTCGGACATTGGAGCACTAAATGAACCTGAATTGTGTCTGTGGCGAGCAGGATGGTCGCTG  
TTACTTTGTATGAGATCGGGGATGAATTGCTCGCTTAAAAATGCTGCTTGGATTCTGTT  
GCTGGAGACGTCTCTTGCCGCTGGAAACGTTACAGGGGACGTTGCAAAGAGAAGA  
TCTGTTCTGCAATGAGATAGAAGGGACCTACACGTAGACTGTGAAAAAAAGGGCTTCACA  
AGTCTGCAGCGTTCACTGCCCGACTTCCCAGTTACCATTTATTCATGGCAATT  
CCTCACTCGACTTTCCCTAATGAGTTCGCTAACCTTATAATGCGGTTAGTTGCACATGG  
AAAACAATGGCTTGCATGAAATCGTCCGGGGCTTTCTGGGCTGCAGCTGGTAAAAGG  
CTGCACATCAACAACAAGATCAAGTCTTTCGAAAGCAGACTTTCTGGGCTGGACGA  
TCTGGAATATCTCCAGGCTGATTTAATTATTACGAGATATAGACCCGGGGCCTCCAGG  
ACTTGAACAAGCTGGAGGTGCTCATTTAAATGACAATCTCATCAGCACCCCTACCTGCCAAC  
GTGTTCCAGTATGTGCCATACCCACCTCGACCTCCGGTAACAGGCTGAAAACGCTGCC  
CTATGAGGAGGTCTGGAGCAAATCCCTGGTATTGCGGAGATCCTGCTAGAGGATAACCC  
GGGACTGCACCTGTGATCTGCTCTCCCTGAAAGAATGGCTGGAAAACATTCCAAGAATGCC  
CTGATCGGCCGAGTGGTCTGCGAAGCCCCCACCAGACTGCAGGGTAAAGACCTCAATGAAAC  
CACCGAACAGGACTTGTGCTTGGAAAAACCGAGTGGATTCTAGTCTCCGGCGCCCCCTG  
CCCAAGAAGAGACCTTGCCTGGACCCCTGCCAACTCCTTCAAGACAAATGGCAAGAG  
GATCATGCCACACCAGGGTCTGCTCCAAACGGAGGTACAAAGATCCCAGGCAACTGGCAGAT  
CAAATCAGACCCACAGCAGCGATAGCGACGGTAGCTCAGGAACAAACCTTAGCTAAC  
GTTTACCTGCCCTGGGGCTGCAGCTGCACCACATCCAGGGTGGTTAAAGATGAAC  
TGCAACAACAGGAACGTGAGCAGCTGGCTGATTGAAGCCAAGCTCTAACGTGCAGGA  
GCTTTCTACGAGATAACAGATCCACAGCATCCGAAAATCGACTTTGTGGATTACAAGA  
ACCTCATTCTGTTGGATCTGGCAACAATAACATCGCTACTGTAGAGAACAAACACTTCAAG  
AACCTTTGGACCTCAGGTGGTATACATGGATAGCAATTACCTGGACACGCTGTCCC  
GAAATTGCGGGGCTGCAAAACCTAGAGTACCTGAACGTGGAGTACAACGCTATCCAGCTCA  
TCCTCCGGCACTTCAATGCCATGCCAAACTGAGGATCCTCATTCTCAACAACAAACCTG  
CTGAGGTCCCTGCCTGTGGACGTGTTCGCTGGGTCTCGCTCTAAACTCAGCCTGCACAA  
CAATTACTCATGTACCTCCGGTGGCAGGGGTGCTGGACCAAGTTAACCTCCATCATCC  
TAGACCTCCACGGAAACCCCTGGAGTGCTCCTGCACAATTGTGCCCTTCAAGCAGTGGCA  
GAACGCTTGGGTTCCGAAGTGTGATGAGCGACCTCAAGTGTGAGACGCCGGTGAACCTT  
TAGAAAGGATTTCATGCTCCTCCAATGACGAGATCTGCCCTCAGCTGTACGCTAGGATCT  
CGCCCACGTTAACCTCGCACAGTAAAACAGCACTGGGTTGGCGGAGACGGGACGCACTCC  
AACTCCTACCTAGACACCAGCAGGGTGTCCATCTCGGTGTTGGTCCGGACTGCTGCTGG  
GTTTGTACCTCCGCCCTCACCGTGGGGCATGCTCGTGTATCCTGAGGAACCGAAAGC  
GGTCCAAGAGACGAGATGCCAACTCCTCCGCTCCGAGATTAATTCCCTACAGACAGTCTGT  
GAECTTCTACTGGCACAATGGCCTTACAACGAGATGGGCCACAGAGTGTATGACTG  
TGGCTCTCACTCGCTCAGACTAACGACCCCAACCCCAATAGGGGAGGGCAGAGGGAAAGGCG  
ATACATCCTCCCCACCGCAGGCACCCCGGGGCTGGAGGGGCGTGTACCCAAATCCCC  
CCATCAGCCTGGATGGGCATAAGTAGATAAAACTGTGAGCTCGCACAACGAAAGGGC  
GACCCCTTACTTAGCTCCCTCCTGAAACAAAGAGCAGACTGTGGAGAGCTGGAGAGCGCA  
GCCAGCTCGCTTTGCTGAGAGCCCCTTGACAGAAAGCCAGCACGACCCCTGCTGGAG  
AACTGACAGTGCCTCGCCCTGGCCCCGGGCTGTGGGGTTGGATGCCGGTTCTATAC  
ATATATACATATATCCACATCTATATAGAGAGATAGATATCTATTTCCTGTGGATTAG  
CCCCGTGATGGCTCCCTGTTGGCTACGCAAGGATGGCAGTTGCACGAAGGCATGAATGTAT  
TGTAAATAAGTAACCTTGACTTCTGAC

## **FIGURE 34**

MLLWILLLETSLCFAAGNVTDVCKEKICSCNEIEGDLHVDCEKKGFTSLQRFTA  
LFLHGNSLTRLFPNEFANFYNAVSLHMENNGLHEIVPG AFLGLQLVKRLHINNNKIKSFRKQ  
TFLGLDDLEYLQADFNLLRIDPGAFQDLNKLEV LILNDNLISTL PANVQYVPITHLDLRG  
NRLKTL PYEEVLEQIPGIAEILLEDNPWDCTCDLLSLKEWLENIPKNALIGRVVCEAPTRLQ  
GKDILNETTEQDLCPLKNRVDSSL PAPPAQEETFAPGPLPTPFKTNGQEDHATPGSAPNGGT  
IPGNWQIKIRPTAAIATGSSRNKPLANSLPCPGGCSDHIPGSGLKMNCNNRNVSSLADLK  
KLSNVQELFLRDNKIHSIRKSHFVDYKNLILL DLGNNNIATVENNTFKNLLDLRWLYMDSNY  
LDTLSREKFAGLQNLEYLNVEYN A IQLILPGTFNAMPKL RILILNNNLLRSLPVDVFAGVSL  
SKLSLHN NYFMYLPVAGVLDQLTSIIQIDLHGNPWECSCTIVPKQWAERLGSEVLMSDLKC  
ETPVNFFRKDFM LLSNDEICPQLYARISPTLTSHSKNSTGLAETGTHSNSYLDTSRVSISVL  
VPGLL VFVTS AFTVVGMLV FILRNRKRSKRRDANSSASEINSLQTVCDSSYWHNGPYNADG  
AHRVYDCGSHSLSD

**Signal sequence:**

amino acids 1-15

**Transmembrane domain:**

amino acids 618-638

**N-glycosylation site.**

amino acids 18-22, 253-257, 363-367, 416-420, 595-599, 655-659

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 122-126, 646-650

**Casein kinase II phosphorylation site.**

amino acids 30-34, 180-184, 222-226, 256-260, 366-370, 573-577,  
608-612, 657-661, 666-670, 693-697

**N-myristoylation site.**

amino acids 17-23, 67-73, 100-106, 302-308, 328-334, 343-349,  
354-360, 465-471, 493-499, 598-604, 603-609

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 337-348

## **FIGURE 35**

AGTCGACTGGTCCCCGTACCCGGGCCAGCTGTGTTCTGACCCCAGAATAACTCAGGGC  
TGCACCGGGCCTGGCAGCGCTCCGCACACATTTCTGTGCGGCCCTAACGGAAACTGTTGGC  
CGCTGGGCCCGGGGGATTCTTGGCAGTTGGGGTCCGTGGAGCGAGGGCGGAGGGG  
AAGGGAGGGGGAACCGGGTGGGAAGCCAGCTGTAGAGGGCGGTGACCGCGCTCCAGACAC  
AGCTCTGCGTCCTCGAGCGGGACAGATCCAAGTGGGAGCAGCTCTCGTGCCTGGGGCCTCAG  
**AGAATGAGGCCGGCGTTGCCCTGTGCCTCCTGGCAGGCCTCTGGCCCTGGGGCCTGCTACAGCCTGC**  
CGGCGAACACCCCACTGCCGACCGTGCTGGCTGGCCTCGGGGGCCTGCTACAGCCTGC  
ACCACGCTACCATGAAGCGGCAGCGGCCGAGGAGGCCTGCATCCTGCGAGGTGGGGCGCTC  
AGCACCGTGCCTGGGGCGCCAGCTGCCTGCTGCTCGCCTCTGCGGGCAGGCCAGG  
GCCCGGAGGGGGCTCAAAGACCTGCTGTTCTGGTGCACGGAGCGCAGGCGTTCCACT  
GCACCCCTGGAGAACGAGCCTTGCAGGGTTCTCCTGGCTGTCCCTCGACCCCGGGCTC  
GAAAGCGACACGCTGCAGTGGGTGGAGGAGCCCCAACGCTCCTGCACCGCGGGAGATGCGC  
GGTACTCCAGGCCACCGGTGGGTGAGGCCGAGGCTGGAAGGAGATGCGATGCCACCTGC  
GCGCCAACGGTACCTGTGCAAGTACCAAGTTGAGGTCTGTGCTCGCCCGCCCCGG  
GCCGCCTTAACCTGAGCTATCGCGCCCTTCAGCTGCACAGCGCGCTCTGGACTTCAG  
TCCACCTGGGACCGAGGTGAGTGCCTGCGCTGGGACAGCTCCCGATCTCAGTTACTGCA  
TCGCGGACGAAATCGGCGCTCGCTGGGACAAACTCTCGGGCGATGTGTTGTCCCTGCC  
GGGAGGTACCTCCGTGGCAAATGCGCAGAGCTCCCTAACGCTCTAGACGACTTGGGAGG  
CTTTCCTGCGAATGTGCTACGGGCTTCGAGCTGGGAAGGACGGCGCTTTGTGACCA  
GTGGGGAGGACAGCCGACCCCTGGGGGACCGGGGTGCCACCAAGGCGCCGCCACT  
GCAACCAGCCCCGTGCCGAGAGAACATGGCAATCAGGGTCGACGAGAACGACTGGGAGAGAC  
ACCACCTGTCCCTGAACAAGACAATTCAAGTAACATCTATTCTGAGATTCTCGATGGGAT  
CACAGAGCACGATGTCTACCCCTCAAATGTCCCTCAAGCCGAGTCAAAGGCCACTATCACC  
CCATCAGGGAGCGTGATTCCAAGTTAACCTACGACTCCCTGCCACTCCTCAGGCTTT  
CGACTCCTCCCTGCCGTGGTCTTCATATTGTGAGCACAGCAGTAGTAGTGTGATCT  
TGACCATGACAGTACTGGGCTTGTCAAGCTCTGCTTCACGAAAGCCCTTTCCAGCCA  
AGGAAGGAGTCTATGGGCCGCCCTGGAGAGTGTACCTGAGCCGCTGCTTGGGCTC  
CAGTCTGCACATTGACAAACAATGGGTGAAAGTCGGGACTGTGATCTGCCAGAG  
CAGAGGGTGCCTTGCTGGCGAGTCCCTCTGGCTCTAGTGATGCAT**AGGGAAACAGGGGA**  
CATGGGCACTCCTGTGAACAGTTTCACTTTGATGAAACGGGAAACCAAGAGGAACCTAC  
TTGTGTAAGTACAATTCTGCAGAAATCCCCCTCCTCTAAATTCCCTTACTCCACTGAG  
GAGCTAAATCAGAACTGCACACTCCTCCCTGATGATAGAGGAAGTGGAAAGTGCCTTAGGA  
TGGTGTACTGGGGACGGGTAGTGCTGGGAGAGATATTCTATGTTATTGGAGAA  
TTTGGAGAAGTGATTGAACCTTCAAGACATTGAAACAAATAGAACACAATATAATTACA  
TTAAAAAATAATTCTACCAAAATGGAAAGGAAATGTTCTATGTTAGGCTAGGAGTAT  
ATTGGTTGAAATCCCAGGGAAAAAATAAAAATTAAAGGATTGTTGAT

## **FIGURE 36**

MRPAFALCLLWQALWPAGPGGGEHPTADRAGCSASGACYSLHHATMKRQAAEACILRGGALS  
TVRAGAELRAVLALLRAGPGPGGGSKDLLFWVALERRSHTLENEPLRGFSWLSSDPGGLE  
SDTLQWVEEPQRSCTARRCAVLQATGGVEPAGWKEMRCHLRANGYLCKYQFEVLCAPRPGA  
ASNLSYRAPFQLHSAALDFSPPGTEVSALCRGQLPISVTCIADEIGARWDKLSGDVLCPCPG  
RYLRAGKCAELPNCLDDLGGFACECATGFELGKDGRSCVTSGEGQPTLGGTGVPTRRPPATA  
TSPVPQRTWPIRVDEKLGETPLVPEQDNSVTSIPEIPRWGSQSTMSTLQMSLQAESKATITP  
SGSVISKFNSTTSSATPQAFDSSSAVVIFVSTAVVVLVILMTVLGLVKLCFHESPSSQPR  
KESMGPPGLES DPEPAALGSSSAHCTNNGVKVGDCDLRDRAEGALLAESPLGSSDA

**Signal sequence:**

amino acids 1-16

**Transmembrane domain:**

amino acids 399-418

**N-glycosylation site.**

amino acids 189-193, 381-385

**Glycosaminoglycan attachment site.**

amino acids 289-293

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 98-102, 434-438

**Casein kinase II phosphorylation site.**

amino acids 275-279, 288-292, 342-346, 445-449

**N-myristoylation site.**

amino acids 30-36, 35-41, 58-64, 59-65, 121-127, 151-157,  
185-191, 209-215, 267-273, 350-356, 374-380, 453-459, 463-469,  
477-483

**Aspartic acid and asparagine hydroxylation site.**

amino acids 262-274

## **FIGURE 37**

CGGACGGCTGGGATTCAAGCAGTGGCTGTGGCTGCCAGAGCAGCTCCTCAGGGAAACTAAG  
CGTCGAGTCAGACGGCACCATATCGCCTTAAAAGTGCCTCCGCCCTGCCGGCGCGTATC  
CCCCGGCTACCTGGGCCCGCCCGCGCGGTGCGCGTGAAGAGGGAGCGCGCGGGCAGCCGA  
GCGCCGGTGTGAGCCAGCGCTGCTGCCAGTGTGAGCGGCCGTGTGAGCGCGTGGGTGCGGA  
GGGGCGTGTGCGCGCGCGCGTGGGTGCAAACCCGAGCGTCTACGCTGCCATGA  
GGGGCGCGAACGCCTGGCGCCACTCTGCCTGCTGGCTGCCGCCACCCAGCTCTCGCGG  
CAGCAGTCCCCAGAGAGACCTGTTTACATGTGGTGGCATTCTTACTGGAGAGTCTGGATT  
TATTGGCAGTGAAGGTTTCTGGAGTGTACCCCTCCAAATAGCAAATGTACTTGGAAAATCA  
CAGTTCCCAGGAAAAGTAGTCGTTCTCAATTCCGATTCAAGACCTCGAGAGTGACAAC  
CTGTGCCGCTATGACTTTGTGGATGTGTACAATGCCATGCCATGGCCAGCGCATTGGCG  
CTTCTGTGGCACTTCCGGCTGGAGCCCTGTGTCCAGTGGCAACAAGATGATGGTGCAGA  
TGATTCTGATGCCAACACAGCTGGCAATGGCTCATGGCCATGTTCTCCGCTGCTGAACCA  
AACGAAAGAGGGATCAGTATTGTGGAGGACTCCTGACAGACCTCCGGCTTTAAAAC  
CCCCAACTGGCCAGACGGGATTACCTGCAGGAGTCACCTGTGTGGCACATTGTAGCCC  
CAAAGAATCAGTTATAGAATTAAAGTTGAGAAGTTGATGTGGAGCGAGATAACTACTGC  
CGATATGATTATGTGGCTGTGTTAATGGCGGGAAAGTCAACGATGCTAGAAGAATTGGAAA  
GTATTGTGGTGTAGTCCACCTGCGCCAATTGTGCTGTGAGAGAAATGAACTTCTTATTCA  
TTTATCAGACTTAAGTTAAC TGCAAGATGGTTATTGGTCACTACATATTCAAGGCCAAA  
AAACTGCCTACAACACAGAACAGCCTGTCACCACCATTCCTGTAACCACGGTTAAA  
ACCCACCGTGGCCTTGTGTCACAAAAGTGTAGACGGACGGGACTCTGGAGGGCAATTATT  
GTTCAAGTGAATTGTATTAGCCGGACTGTTACACACCACACTCGCGATGGGAGTTG  
CACGCCACAGTCTCGATCATCAACATCTACAAAGAGGGAAATTGGCGATT CAGCAGGCC  
CAAGAACATGAGTGCCAGGCTGACTGTCGTGCAAGCAGTGCCCTCTCCTCAGAAGAGGTC  
TAAATTACATTATTATGGCCAAGTAGGTGAAGATGGCGAGGCAAATCATGCCAACAGC  
TTTATCATGATGTTCAAGACCAAGAACATCAGAACGCTCCTGGATGCCCTAAAAAATAAGCAATG  
TTAACAGTGAACTGTGTCATTAAAGCTGTATTCTGCCATTGCCCTTGAAAGATCTATGTC  
TCTCAGTAGAAAAAAATACTTATAAAATTACATATTCTGAAAGAGGATTCCGAAAGATGG  
GACTGGTTGACTCTTCACATGATGGAGGTATGAGGCCTCCGAGATAGCTGAGGGAAAGTTCTT  
TGCCCTGCTGTCAGAGGAGCAGCTATCTGATTGGAAACCTGCCGACTTAGTGCCTGATAGGA  
AGCTAAAAGTGTCAAGCGTTGACAGCTTGGAAAGCGTTATTATACATCTGTAAAAGGAT  
ATTTAGAATTGAGTTGTGTGAAGATGTCAAAAAAAGATTAGAAGTGCAATATTATAGT  
GTTATTTGTTCACCTCAAGCCTTGCCCTGAGGTGTTACAATCTGTCTGCCTTCTA  
AATCAATGCTTAATAAAATATTAAAGGAAAAAA

## **FIGURE 38**

MRGANAWAPLCLLLAAATQLSRQSPERPVFTCGGILTGESGFIGSEGFPGVYPPNSKCTWK  
ITVPEGKVVVLNFRFIDLESDNLCRYDFVDVYNGHANGQRIGRFCGTFRPGALVSSGNKMMV  
QMISDANTAGNGFMAMFSAAEPNERGDQYCGGLDRPSGSFKTPNWPDYPAVGTCVWHIV  
APKNQLIELKFEKFDVERDNYCRYDYVAVFNGEVNDARRIGKYCGDSPPAPIVSERNELLI  
QFLSDLSSLTADGFIGHYIFRPKKLPTTTEQPVTTFPVTTGLKPTVALCQQKCRRTGTLEGN  
YCSSDFVLAGTVITTITRDGSLHATVSIINIYKEGNLAIQQAGKNMSARLTVVCKQCPLLRR  
GLNYIIMQVGEDGRGKIMPNSFIMMFTKNQKLLDALKNKQC

**Signal sequence:**

amino acids 1-23

**N-glycosylation site.**

amino acids 355-359

**Casein kinase II phosphorylation site.**

amino acids 64-68, 142-146, 274-278

**Tyrosine kinase phosphorylation site.**

amino acids 199-208

**N-myristoylation site.**

amino acids 34-40, 35-41, 100-106, 113-119, 218-224, 289-295,  
305-311, 309-315, 320-326, 330-336

**Cell attachment sequence.**

amino acids 149-152

## **FIGURE 39**

CGGACCGCGTGGCGGGACCGCGTGGCGGCCACGGCGCCCGGGCTGGGCGGTGCCTTCTT  
CCTTCTCCGTGGCTACGAGGGTCCCCAGCCTGGTAAAGATGGCCCCATGGCCCCGAAGG  
GCCTAGTCCCAGCTGTGCTCTGGGCCTCAGCCTCTTCACACCTCCAGGACCTATCTGG  
CTCCAGCCCTCTCCACCTCCCCAGTCTTCTCCCCGCCTCAGCCCCATCCGTGTACACCTG  
CCGGGGACTGGTTGACAGCTTAACAAGGGCCTGGAGAGAACCATCCGGACAACTTGGAG  
GTGGAAACACTGCCTGGGAGGAAGAGAATTGTCAAATACAAAGACAGTGAGACCCGCCTG  
GTAGAGGTGCTGGAGGGTGTGCAGCAAGTCAGACTTCGAGTGCCACCGCCTGCTGGAGCT  
GAGTGAGGAGCTGGTGGAGAGCTGGTGGTTCACAAAGCAGCAGGAGGCCGGACCTCTCC  
AGTGGCTGTGCTCAGATTCCCTGAAGCTCTGCTGCCCGCAGGCACCTCGGGCCCTCCTGC  
CTTCCCTGTCTGGGAAACAGAGAGGCCCTGCGGTGGCTACGGGCAGTGAGGAGAAGG  
GACACGAGGGGGCAGCGGGCACTGTGACTGCCAAGCCGGTACGGGGTGAGGCCTGTGGCC  
AGTGTGGCCTGGCTACTTGAGGCAGAACGCAACGCCAGCCATCTGGTATGTTGGCTTGT  
TTTGGCCCTGTGCCGATGCTCAGGACCTGAGGAATCAAACGTGGCAATGCAAGAAGGG  
CTGGGCCCTGCATCACCTCAAGTGTAGACATTGATGAGTGAGGCACAGAGGGAGCCA  
GTGGAGCTGACCAATTCTCGTGAACACTGAGGGCTCCTATGAGTGCCGAGACTGTGCCAAG  
GCCTGCCTAGGCTGCATGGGGCAGGGCCAGGTCGCTGTAAGAAGTGTAGCCCTGGCTATCA  
GCAGGTGGCTCCAAGTGTCTCGATGGATGAGTGAGACAGAGGTGTCCGGAGAGA  
ACAAGCAGTGTAAAACACCGAGGGCGTTATCGCTGCATCTGTGCCGAGGGCTACAAGCAG  
ATGGAAGGCATCTGTGTGAAGGAGCAGATCCCAGAGTCAGCAGGCTTCTCAGAGATGAC  
AGAAGACGAGTTGGTGGTGCTGCAGCAGATGTTCTTGGCATCATCATCTGTGCACTGGCA  
CGCTGGCTGCTAAGGGCAGTTGGTGTACCGCCATCTCATTGGGCTGTGGCGGCCATG  
ACTGGCTACTGGTTGTCAAGAGCGCAGTGACCGTGTGGAGGGCTTCATCAAGGGCAGATA  
ATCGCGGCCACCACCTGTAGGACCTCCCACCCACGCTGCCCGAGAGCTTGGCTGCC  
TCCTGCTGGACACTCAGGACAGCTTGGTTATTTTGAGAGTGAGGTAAAGCACCCCTACCTG  
CCTTACAGAGCAGCCCAGGTACCCAGGCCGGCAGACAAGGCCCTGGGTAAAAGTAGC  
CCTGAAGGTGGATACCATGAGCTCTCACCTGGGGGGACTGGCAGGCTTCACAATGTGTGA  
ATTTCAAAAGTTTCTTAATGGTGGCTGCTAGAGCTTGGCCCTGCTTAGGATTAGGTG  
GTCCTCACAGGGTGGGCCATCACAGCTCCCTGCCAGCTGCATGCCAGTTCTGT  
TCTGTGTTACCCACATCCCCACACCCATTGCCACTTATTATTCATCTCAGGAAATAAGA  
AAGGTCTTGGAAAGTTAAAAAAAAAAAAAAA

## **FIGURE 40**

MAPWPPKGLVPAVLWGLSLFLNLPGPIWLQPSPPPQQSSPPQPHPCHTCRGLVDSFNKGLER  
TIRDNFGGGNTAWEEENLSKYKDSETRLVEVLEGVCSKSDFECHRLLESELVESWWFHKQ  
QEAPDLFQWLCSDSLKLCGPAGTFGPGSCLPCPGGTERPCGGYGCCEGEGTRGGSGHCDCQAG  
YGGECACGQCGGLGYFEAERNASHLVCACFGPCARCSGPEESNLQCKKGWALHHLKCVDIDE  
CGTEGANCGADQFCVNTEGSYECRDCAKACLGCMGAGPGRCKCSPGYQQVGSKCLDVDECE  
TEVCPGENKQCENTEGGYRCICAEGYKQMEGICVKEQIPESAGFFSEMTEDELVVLQQMFFG  
IIICALATLAKGDLVFTAIFIGAVAAMTGYWLRSDRVLEGFIKGR

**Signal sequence:**

amino acids 1-29

**Transmembrane domain:**

amino acids 372-395

**N-glycosylation site.**

amino acids 79-83, 205-209

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 290-294

**Casein kinase II phosphorylation site.**

amino acids 63-67, 73-77, 99-103, 101-105, 222-226, 359-263

**N-myristoylation site.**

amino acids 8-14, 51-57, 59-65, 69-75, 70-76, 167-173, 173-179,  
177-183, 188-194, 250-256, 253-259, 267-273, 280-286, 283-289,  
326-332, 372-378, 395-401

**Aspartic acid and asparagine hydroxylation site.**

amino acids 321-333

**EGF-like domain cysteine pattern signature.**

amino acids 181-193

## **FIGURE 41**

TGAGACCCTCCTGCAGCCTCTCAAGGGACAGCCCCACTCTGCCTCTTGCTCCCTCCAGGGCA  
GCACCATGCCAGCCCCTGTGGCTCTGCTGGGCACTCTGGGTGTTGCCCTGCCAGCCCCGGG  
GCCGCCCTGACCGGGGAGCAGCTCCTGGCAGCCTGCTGCCAGCTGCAGCTCAAAGAGGT  
GCCCACCCCTGGACAGGGCCGACATGGAGGAGCTGGTCATCCCCACCCACGTGAGGGCCAGT  
ACGTGGCCCTGCTGCAGCGCAGCCACGGGACCGCTCCCGGGAAAGAGGTTCAGCCAGAGC  
TTCCGAGAGGTGGCCGGCAGGTTCCCTGGCGTTGGAGGCCAGCACACACCTGCTGGTGGTCGG  
CATGGAGCAGCGGCTGCCGCCAACAGCGAGCTGGTGAGGCCGTGCTGCCGTCTTCCAGG  
AGCCGGTCCCCAAGGCCGCGCTGCACAGGCACGGGCGGCTGTCCCCGCGCAGGCCGGGCC  
CGGGTACCGTCGAGTGGCTGCCGTCCACGAGAGCGGCTGGAAGGCCTTCGACGTGACCGAGGCCGTGA  
ACTTCTGGCAGCAGCTGAGCCGGCCCCGGCAGCCGCTGCTGCTACAGGTGTCGGTGCAGAGG  
GAGCATCTGGCCCGCTGGCGTCCGGCCACAAGCTGGTCCGCTTGCCCTCGCAGGGGC  
GCCAGCCGGCTTGGGAGCCCCAGCTGGAGCTGCACACCCCTGGACCTTGGGACTATGGAG  
CTCAGGGCAGCTGTGACCCCTGAAGCACCAATGACCGAGGGCACCCGCTGCTGCCGCCAGGAG  
ATGTACATTGACCTGCAGGGATGAAGTGGCCGAGAACTGGGTGCTGGAGGCCCGGGCTT  
CCTGGCTTATGAGTGTGGCACCTGCCGGCAGCCCCGGAGGCCCTGGCCTTAAGTGGC  
CGTTCTGGGCCTCGACAGTCATGCCCTGGAGACTGACTCGCTGCCATGATCGTCAGC  
ATCAAGGAGGGAGGCAGGACCAGGCCAGGTGGTCAGCCTGCCAACATGAGGGTGCAGAA  
GTGCAGCTGTGCCTCGATGGTGCCTCGTGCCTAGGCCAAGGAGGCTCCAGCCATAGGCGCTAGTG  
TAGCCATCGAGGGACTTGACTTGTGTGTTCTGAAGTGGTGCAGGGTACAGGAGAGCTG  
GCGATGACTGAAGTGCCTGATGGACAAATGCTCTGTGCTCTAGTGAGCCCTGAATTGCTT  
CCTCTGACAAGTTACCTCACCTAATTTGCTCTCAGGAATGAGAATCTTGGCCACTGGA  
GAGCCCTGCTCAGTTCTCTATTCTATTCACTGCACTATATTCTAACACTTACAT  
GTGGAGATACTGTAACCTGAGGGCAGAAAGCCANTGTGTCATTGTTACTGTGTCCTGTCAC  
TGGATCTGGCTAAAGTCCTCCACCACACTGGACCTAACAGACCTGGGTTAAGTGTGGGT  
TGTGCATCCCCAATCCAGATAATAAGACTTTGAAAACATGAATAAACACACATTATTCT  
AAAA

## **FIGURE 42**

MQPLWLCWALWVLPLASPGAAALTGEQLLGSLRQLQLKEVPTLDRADMEELVIPTHVRAQYV  
ALLQRSHGDRSRGKRFQSFRREVAGRFLALEASTHLLVFGMEQRLPPNSELVQAVLRLFQEP  
VPKAALHRHGRLSPRSARARVTVEWLVRDDGSNRTSLIDSRLVSHESGWKAFDVTEAVNF  
WQQLSRPRQPLLQSVQREHLGPLASGAHKLVRFASQGAPAGLGEPQLELHTLDLGDYGAQ  
GDCDPEAPMTEGTRCCRQEMYIDLQGMKWAENWVLEPPGFLAYECVGTCRQPPEALAFKWPF  
LGPRQCIASETDSLPMIVSIKEGGRTQPVVSLPNMRVQKCSCASDGALVPRRLQP

**Signal sequence:**

amino acids 1-18

**N-glycosylation site.**

amino acids 158-162

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 76-80

**Casein kinase II phosphorylation site.**

amino acids 68-72, 81-85, 161-165, 169-173, 319-323, 329-333

**N-myristoylation site.**

amino acids 19-25, 156-162, 225-231, 260-266, 274-280

**Amidation site.**

amino acids 74-78

**TGF-beta family signature.**

amino acids 282-298

## **FIGURE 43**

GTCTGTTCCCAGGAGTCCTCGCGGCTGTTGTCACTGGCCTGATCGCGATGGGACAAA  
GGCGCAAGTCGAGAGGAAACTGTTGTGCCTCTCATATTGGCGATCCTGTTGTGCTCCCTGG  
CATTGGGCAGTGTACAGTGCACCTCTGAACCTGAAGTCAGAATTCCCTGAGAATAATCCT  
GTGAAGTTGTCTGTGCCACTCGGGCTTTCTTCTCCCCGTGTGGAGTGGAAAGTTGACCA  
AGGAGACACCACCAGACTCGTTGCTATAATAACAAGATCACAGCTCCTATGAGGACCGGG  
TGACCTTCTTGCCAACGGTATCACCTCAAGTCCGTACACGGGAAGACACTGGGACATAC  
ACTTGTATGGTCTCTGAGGAAGGCGAACAGCTATGGGGAGGTCAAGGTCAAGCTCATCGT  
GCTTGTGCCCTCATCCAAGCCTACAGTTAACATCCCTCCTGCCACCATTGGGAACCGGG  
CAGTGCTGACATGCTCAGAACAGATGGTCCCCACCTTCTGAATAACACACTGGTTCAAAGAT  
GGGATAGTGTGCTACGAATCCAAAAGCACCCGTGCCCTCAGCAACTCTCCTATGTCCT  
GAATCCCACAAACAGGAGAGCTGGTCTTGATCCCTGTCAAGCTCTGATAACTGGAGAATACA  
GCTGTGAGGCACGGAATGGGTATGGGACACCCATGACTCAAATGCTGTGCGCATGGAAAGCT  
GTGGAGCGGAATGTGGGGTCATCGTGGCAGCCGTCTTGTAAACCTGATTCTCCTGGGAAT  
CTTGGTTTTGGCATCTGGTTGCCTATAGCCGAGGCCACTTGACAGAACAAAGAAAGGGA  
CTTCGAGTAAGAAGGTGATTACAGCCAGCCTAGTGCCGAAGTGAAGGAGAATTCAAACAG  
ACCTCGTCATTCTGGTGTGAGCCTGGTCGGCTACCGCCTATCATCTGCATTGCCTTACT  
CAGGTGCTACCGACTCTGGCCCTGATGTCTGTAGTTCACAGGATGCCTTATTGTCCT  
TACACCCACAGGGCCCCCTACTTCTCGGATGTGTTTAATAATGTCAGCTATGTGCC  
ATCCTCCTCATGCCCTCCCTCCCTTACCACTGCTGAGTGGCTGGAACTGTTAAA  
GTGTTATTCCCCATTCTTGAGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTCCC  
TTCTAAGTAGACAGAAAAATGGGGGGTCGCAGGAATCTGCACTCAACTGCCACCTGGC  
TGGCAGGGATCTTGAATAGGTATCTTGAGCTGGTCTGGCTCTTCTGTACTGAC  
GACCAGGGCCAGCTGTTCTAGAGCGGGATTAGAGGCTAGAGCGGCTGAAATGGTTGG  
TGATGACACTGGGTCTTCCATCTCTGGGCCACTCTCTCTGTCTTCCATGGAAAGTG  
CCACTGGGATCCCTGCCCCTGCTCTGAATACAAGCTGACTGACATTGACTGTCTGT  
GGAAAATGGGAGCTTGTGGAGAGCATAGTAAATTTCAGAGAACTTGAAGCCAAAAG  
GATTAAAACCGCTGCTCTAAAGAAAAGAAAATGGAGGCTGGCGCAGTGGCTCACGCC  
TAATCCCAGAGGCTGAGGCAGGCAGGATCACCTGAGGTGGAGTTGGGATCAGCCTGACCA  
ACATGGAGAAACCTACTGGAAATACAAAGTTAGCCAGGCATGGTGGTGCATGCCTGTAGTC  
CCAGCTGCTCAGGAGCCTGGCAACAAGAGAAAATCCAGCTCAAAAAAAAAAAAAAA

## **FIGURE 44**

MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPKLSCAYSGFSSPRVEW  
KFDQGDTTRILVCYNNKITASYEDRVTFLPTGITFKSVTREDTGYTCMVSEEGGNSYGEVKV  
KLIVLVPPSKPTVNI PSSATIGNRAVLTCSEQDGSPPSEYTWFKDGI VMPTNPKSTRAFSNS  
SYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIVAAVLVTLI  
LLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPSARSEGEFKQTSSFLV

**Signal sequence:**

amino acids 1-27

**Transmembrane domain:**

amino acids 238-255

**N-glycosylation site.**

amino acids 185-189

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 270-274

**Casein kinase II phosphorylation site.**

amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,  
193-197, 203-207, 287-291

**N-myristoylation site.**

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

## **FIGURE 45**

CAGCGCGTGGCCGGCGCCGCTGTGGGGACAGCATGAGCGCGTTGGATGGCGCAGGTTGGA  
GCGTGGCGAACAGGGGCTCTGGGCCTGGCGCTGCTGCTGCTCGGCCTCGGACTAGGCCT  
GGAGGCCGCGCGAGCCCGCTTCCACCCGACCTCTGCCAGGCCAGGCCAGGCCCCAGCTCAG  
GCTCGTCCCACCCACCAAGTCCAGTGCCGACCAGTGGCTTATGCGTCCCCTCACCTGG  
CGCTGCGACAGGGACTTGGACTGCAGCGATGGCAGCGATGAGGAGGAGTGCAGGATTGAGCC  
ATGTACCCAGAAAGGGCAATGCCACCGCCCCCTGGCCTCCCTGCCCTGCACCGCGTCA  
GTGACTGCTCTGGGGAACTGACAAGAAACTGCGCAACTGCAGCCGCTGGCCTGCCTAGCA  
GGCGAGCTCCGTTGCACGCTGAGCGATGACTGCATTCCACTCACGTGGCGCTGCGACGGCCA  
CCCAGACTGTCCCGACTCCAGCGACGAGCTGGCTGTGGAACCAATGAGATCCTCCCGGAAG  
GGGATGCCACAACCATGGGGCCCCCTGTGACCCCTGGAGAGTGTCACCTCTCAGGAATGCC  
ACAACCATGGGGCCCCCTGTGACCCCTGGAGAGTGTCCCCTGTGCGGAATGCCACATCCTC  
CTCTGCCGGAGACCAGTCTGGAAGGCCAACTGCCTATGGGTTATTGCAGCTGCTGCCGTGC  
TCAGTGCAAGCCTGGTCACGCCACCCCTCCTCCTTGTCCCTGGCTCCGAGGCCAGGAGCGC  
CTCCGCCCACTGGGTTACTGGTGGCCATGAAGGAGTCCCTGCTGTCAGAACAGAACAGAC  
CTCGCTGCCTGAGGACAAGCACTTGCCACCACCGTCACTCAGCCCTGGCGTAGCCGGACA  
GGAGGAGAGCAGTGATGCGGATGGTACCCGGCACACCAGCCCTCAGAGACCTGAGTTCTT  
CTGCCACGTGGAACCTCGAACCCGAGCTCCTGCAGAAGTGGCCCTGGAGATTGAGGGTCCC  
TGGACACTCCCTATGGAGATCCGGGGAGCTAGGATGGGAACCTGCCACAGCCAGAACAGAC  
GGGCTGGCCCCAGGCAGCTCCAGGGGGTAGAACGCCCTGTGCTTAAGACACTCCCTGCTG  
CCCCGTCTGAGGGTGGCGATTAAAGTTGCTTC

## **FIGURE 46**

MSGGWMAQVGAWRTGALGLALLLGLGLEAAASPLSTPTSAQAAGPSSGSCPPTKFQCR  
TSGLCVPLTWRCRDLD CSDGSDEEECRIEPCTQKGQC PPPGLPCPCTGVSDCSGGDKKL  
RNC SRLA CLAGELRCTL SDDCIPLTWRC DGH PDCP DSS DEL GCGTNEILPEGDATTMGPPVT  
LES VTS LRN ATT MGPP VT LES VPS VGNAT SSS AGD QSGS PTAY GVIAAAAV LS AS LVT AT LL  
LL SWL RAQER LRPL GLLVAM KESLLL SEQ KTS LP

**Signal sequence:**

amino acids 1-30

**Transmembrane domain:**

amino acids 230-246

**N-glycosylation site.**

amino acids 126-130, 195-199, 213-217

**Casein kinase II phosphorylation site.**

amino acids 84-88, 140-144, 161-165, 218-222

**N-myristoylation site.**

amino acids 3-9, 10-16, 26-32, 30-36, 112-118, 166-172, 212-218,  
224-230, 230-236, 263-269

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 44-55

**Leucine zipper pattern.**

amino acids 17-39

## **FIGURE 47**

CCACCGCGTCCGGTCTCGCTCGCGCAGCGGCGGCAGCAGAGGTGCCACAGATGCGG  
GTTAGACTGGCGGGGGAGGAGGCGGAGGAGGAAGGAAGCTGCATGCATGAGACCCACAGA  
CTCTGCAAGCTGGATGCCCTCTGTGGATGAAAGATGTTATCATGGAATGAACCCGAGCAATG  
GAGATGGATTCTAGAGCAGCAGCAGCAGCACACCTCAGTCCCCCAGAGACTCTTG  
GCCGTGATCCTGTGGTTTCAGCTGGCGCTGTGCTTCGGCCCTGCACAGCTCACGGCGGGTT  
CGATGACCTCAAGTGTGCTGACCCCGCATTCCGAGAATGGCTTCAGGACCCCCAGCG  
GAGGGGTTTCTTGAAAGGCTCTGTAGCCGATTTCACTGCCAAGACGGATTCAAGCTGAAG  
GGCGCTACAAAGAGACTGTGTTGAAGCATTAAATGGAACCTAGGCTGGATCCAAGTGA  
TAATTCCATCTGTGCAAGAAGATTGCCGTATCCCTCAAATGAAGATGCTGAGATTATA  
ACAAGACATATAGACATGGAGAGAACGTAATCATCACTTGTATGAAGGATTCAAGATCCGG  
TACCCGACCTACACAATATGGTTTCAATTATGTCGCGATGATGGAACGTGGAATAATCTGCC  
CATCTGTCAAGGCTGCCTGAGACCTCTAGCCTCTTAATGGCTATGTAAACATCTCTGAGC  
TCCAGACCTCCTCCCGTGGGACTGTGATCTCCTATCGCTGCTTCCGGATTAAACTT  
GATGGGTCTGCGTATCTTGAGTGCCTACAAAACCTTATCTGGCGTCCAGCCCACCCGGTG  
CCTTGCTCTGGAAGCCAAGTCTGTCCACTACCTCCAATGGTAGTCACGGAGATTCGTCT  
GCCACCCGCGCCTTGTGAGCGTACAACCACGGAACGTGGTGGAGTTTACTGCGATCCT  
GGCTACAGCCTCACCAAGCGACTACAAGTACATCACCTGCCAGTATGGAGAGTGGTTCCCTC  
TTATCAAGTCTACTGCATCAAATCAGAGCAAACGTGGCCAGCACCCATGAGACCCCTCTGA  
CCACGTGGAAGATTGTGGCGTTACGGCAACCAGTGTGCTGGTGTGCTCGTCATC  
CTGGCCAGGATGTTCCAGCCAAGTTCAAGGCCACTTCCCCCAGGGGCTCCCCGGAG  
TTCCAGCAGTGACCTGACTTTGTGGTAGACGGCGTGCCTCATGCTCCGTCTATG  
ACGAAGCTGTGAGTGGCGCTTGAGTGCCTTAGGCCCGGGTACATGGCCTCTGTGGCCAG  
GGCTGCCCTTACCGTGGACGACCAGAGCCCCCAGCATACCCGGCTCAGGGACACGGA  
CACAGGCCAGGGAGTCAGAAACCTGTGACAGCGTCTCAGGCTCTTGAGCTGCTCCAAA  
GTCTGTATTCACCTCCAGGTGCCAAGAGAGCACCCACCCGCTCGGACAACCTGACATA  
ATTGCCAGCACGGCAGAGGAGGTGGCATCCACCAGCCAGGCATCCATCATGCCACTGGGT  
GTTGTTCTAAGAAACTGATTGATTAAAAAATTCCAAAGTGTCTGAAGTGTCTCTCAA  
ATACATGTTGATCTGTGGAGTTGATTCCCTTCTCTTGAGTAAACAA  
AGCTCTGATCTTAAAATTGCTATGCTGATAGAGTGGTAGGGCTGGAAGCTTGATCAAGTC  
CTGTTCTTCTTGACACAGACTGATTAAAATTAAAAGNAAAAAA

## **FIGURE 48**

MYHGMNPSNGDGFLEQQQQQQQQPQSPQRLLAVILWFQLALCFGPAQLTGGFDDLQVCADPGI  
PENGFRTPSGGVFFEGSVARFHQCQDGFKLGATKRLCLKHFNGTLGWIPSDNSICVQEDCRI  
PQIEDAEIHNKTYRHGEKLIITCHEGFKIRYPDLHNMVSLCRDDGTWNNLPICGGCLRPLAS  
SNGYVNISELQTSFPVGTVISYRCFPGFKLDGSAYLECLQNLIWSSSPRCLALEAQVCPLP  
PMVSHGDFVCHPRPCERYNHGTVVEFYCDPGYSLTSDYKYITCQYGEWFPSYQVYCIKSEQT  
WPSTHETLLTWKIVAFATSVLLVLLVILARMFQTKFKAHFPPRGPPRSSSDPDFVVVD  
GVPVMLPSYDEAVSGGLSALGPGYMASVGQGCPLPVDDQSPPAYPGSGD'TDGPGESETCDS  
VSGSSELLQSLYSPPRCQESTHPASDNPDIIASTAEEVASTSPGIHHAHWVLFLRN

**Signal sequence:**

amino acids 1-41

**Transmembrane domain:**

amino acids 325-344

**N-glycosylation site.**

amino acids 104-108, 134-138, 192-196

**Casein kinase II phosphorylation site.**

amino acids 8-12, 146-150, 252-256, 270-274, 313-317, 362-366,  
364-368, 380-384, 467-471, 468-472

**N-myristoylation site.**

amino acids 4-10, 61-67, 169-175, 203-209, 387-393, 418-424,  
478-484

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 394-405

## **FIGURE 49**

CCACCGCGTCCGCTCCGCCTCCCCCCCCGCCTCCCGTGCAGTCGGTCCGTGGCCTAGAGA  
TGCTGCTGCCCGGGTTGCAGTTGTCGCACGCCCTGCCGCCAGCCGCTCCACCGCCGT  
AGCGCCCGAGTGTGGGGGGCGCACCCGAGTCGGGCCATGAGGCGGGAACCGCGCTACAGG  
CCGTGCTGCTGGCGTGCCTGGTGGGCTGCAGGGCGACGGTCGCCTGCTGAGTGCC  
TCGGATTGGACCTCAGAGGAGGGCAGCCAGTCTGCCGGGAGGGACACAGAGGCCTGTTA  
TAAAGTCATTACTTCATGATACTTCTGAAGACTGAACCTTGAGGAAGCCAAGAACGCT  
GCAGGAGGGATGGAGGCCAGCTAGTCAGCATCGAGTCTGAAGATGAACAGAAACTGATAGAA  
AAGTCATTGAAAACCTCTGCCATCTGATGGTACCTCTGGATTGGCTCAGGAGGCCTGA  
GGAGAAACAAAGCAATAGCACAGCCTGCCAGGACCTTATGCTTGGACTGATGGCAGCATAT  
CACAACTTAGAACCTGGTATGTGGATGAGCCGTCCTGCAGCAGGTCTGCGTGGTCATG  
TACCATCAGCCATCGGCACCCGCTGGCATCGAGGCCCTACATGTTCCAGTGGAAATGATGA  
CCGGTGCAACATGAAGAACAAATTTCATTGCAAATATTCTGATGAGAAACCAGCAGTCCTT  
CTAGAGAAGCTGAAGGTGAGGAAACAGAGCTGACAACACCTGTACTTCCAGAAGAACACAG  
GAAGAACATGCCAAAAAAACATTAAAGAAAGTAGAGAACAGCTGCCTGAATCTGGCCTACAT  
CCTAATCCCCAGCATTCCCCTCTCCTCCTGTGGTACCAACAGTGTATGTTGGGTTT  
GGATCTGTAGAAAAAGAAAACGGGAGCAGCCAGACCCCTAGCACAAAGAACACACCATC  
TGGCCCTCTCCTCACCAAGGAAACAGCCGGACCTAGAGGTCTACAATGTATAAGAAAACA  
AAGCGAAGCTGACTTAGCTGAGACCCGGCAGACCTGAAGAATATTCAATTCCGAGTGTGTT  
CGGGAGAAGCCACTCCGATGACATGTCTGTGACTATGACAACATGGCTGTGAACCCATCA  
GAAAGTGGTTGTGACTCTGGTGGAGAGTGGATTGTGACCAATGACATTATGA  
GTTCTCCCCAGACCAAATGGGAGGAGTAAGGAGTCTGGATGGGTGAAAATGAAATATATG  
GTTATTAGGACATATAAAACTGAAACTGACAACAAATGGAAAAGAAATGATAAGCAAAATC  
CTCTTATTTCTATAAGGAAAATACACAGAACGGTCTATGAACAAGCTTAGATCAGGTCTGT  
GGATGAGCATGTGGTCCCCACGACCTCCTGTGGACCCCCACGTTGGCTGTATCCTTAT  
CCCAGCCAGTCATCCAGCTCGACCTTATGAGAACGGTACCTGCCAGGTCTGGCACATAGTA  
GAGTCTCAATAATGTCACTTGGTTGTATCTAACCTTAAGGGACAGAGCTTACCTG  
GCAGTGATAAAAGATGGGCTGTGGAGCTTGGAAAACCACCTCTGTTCTGCTATACAG  
CAGCACATATTATCATAACAGACAGAAAATCCAGAACATCTTCAAAGCCCACATGGTAGCACAG  
GTTGGCCTGTGCATGGCAATTCTCATATCTGTTTTCAAAGAATAAAATCAAATAAAGA  
GCAGGAAAAAA

## **FIGURE 50**

MRPGTALQAVLLAVLLVGLRAATGRLLSASDLRGGQPVCRGGTQRPCYKVIYFHDTSRRL  
NFEEAKEACRRDGGQLVSIESEDEQKLIEKFIENLLPSDGDFWIGLRRREEQSNSTACQDL  
YAWTDGSISQFRNWYVDEPSCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNFICKY  
SDEKPAVPSREAEGEETELTPVLPETQEEDAKKTFKESREAALNLAYILIPSIPLLLL  
VTTVVVCWWICRKRKREQPDPSKKQHTIWPSPHQGNSPDLEVYNVIRKQSEADLAETRPDL  
KNISFRVCSGEATPDDMSCDYDNMAVNPSSEGFTLVSVESGFVTNDIYEFSPDQMGRSKES  
GWVENEIYGY

**Signal sequence:**

amino acids 1-21

**Transmembrane domain:**

amino acids 235-254

**N-glycosylation site.**

amino acids 117-121, 312-316

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 296-300

**Casein kinase II phosphorylation site.**

amino acids 28-32, 30-34, 83-87, 100-104, 214-218, 222-226,  
299-303, 306-310, 323-327

**N-myristoylation site.**

amino acids 18-24, 37-43, 76-82, 146-152

## **FIGURE 51**

GGGGTCTCCCTCAGGCCGGGAGGCACAGCGTCCCTGCTGAAGGGCTGGATGTACGC  
ATCCGCAGGTTCCCGCGGACTTGGGGCGCCCGCTGAGCCCCGGCGCCCGCAGAAGACTTGT  
GTTTGCTCCTGCAGCCTCAACCCGGAGGGCAGCGAGGGCCTACCACCATGATCACTGGTGT  
GTTCAGCATGCGCTTGTGGACCCCAGTGGCGTCTGACCTCGCTGGCGTACTGCCTGCACC  
AGCGGCGGGTGGCCCTGGCGAGCTGCAGGAGGCCATGCCAGTGTCCGGTCACCGCAGC  
CTGCTGAAGTTGAAAATGGTGCAGGTGTTGACACGGGGCTGGAGTCCCTCAAGCC  
GCTCCCGCTGGAGGAGCAGGTAGAGTGGAACCCCCAGCTATTAGAGGTCCCACCCAAACTC  
AGTTGATTACACAGTCACCAATCTAGCTGGTGGTCCGAAACCATAATTCTCCTTACGACTCT  
CAATACCATGAGACCACCCCTGAAGGGGGCATGTTGCTGGCAGCTGACCAAGGTGGCAT  
GCAGCAAATGTTGCCTGGAGAGAGACTGAGGAAGAACTATGTGAAGACATTCCCTTC  
TTTCACCAACCTCAACCCACAGGAGGTCTTATTGTTCCACTAACATTTCGGAATCTG  
GAGTCCACCCGTTGTTGCTGGCTGGCTTTCCAGTGTCAAGAAAGAAGGACCCATCATCAT  
CCACACTGATGAAGCAGATTCAAAGTCTGTATCCAACTACCAAAGCTGGAGCCTGA  
GGCAGAGAACCAAGAGGCCGGAGGCAGACTGCCTCTTACAGCCAGGAATCTCAGAGGATTG  
AAAAAGGTGAAGGACAGGATGGCATTGACAGTAGTGTATAAGTGGACTTCTCATCCTCCT  
GGACAACGTGGCTGCCGAGCAGGCACACAACCTCCAAGCTGCCCATGCTGAAGAGATTG  
CACGGATGATCGAACAGAGAGCTGTGGACACATCCTGTACATACTGCCAAGGAAGACAGG  
GAAAGTCTTCAGATGGCAGTAGGCCATTCCCTCACATCCTAGAGAGCAACCTGCTGAAAGC  
CATGGACTCTGCCACTGCCCGACAAGATCAGAAAGCTGTATCTCTATGGGGCTCATGATG  
TGACCTTCATACCGCTTTAATGACCTGGGGATTTTGACCACAAATGCCACCGTTGCT  
GTTGACCTGACCATGGAACCTTACCAAGCACCTGGAATCTAAGGAGTGGTTGTGCAGCTCTA  
TTACCAACGGGAAGGAGCAGGTGCCGAGAGGTTGCCCTGATGGGCTCTGCCCGCTGGACATGT  
TCTTGAATGCCATGTCAGTTACCTTAAGCCCAGAAAAATACCATGCACTCTGCTCTCAA  
ACTCAGGTGATGGAAGTTGGAAATGAAGAGTACTGATTATAAAAGCAGGATGTGTTGATT  
TTAAAATAAAAGTGCCTTATACAATG

## **FIGURE 52**

MITGVFSMRLWTPVGVLTSLAYCLHQRRVALAELOEADGQCPVDRSLLKLKMVQVVFRHGAR  
SPLKPLPLEEQVEWNPQLLEVPPQTQFDYTVTNLAGGPKPYSPYDSQYHETTLKGGMFAGQL  
TKVGMQQMFALGERLRKNYVEDIPFLSPTFNQEVFIRSTNIFRNLESTRCLLAGLFQCQKE  
GPIIIHTDEADSEVLYPNYQSCWSLRQRTRGRQTAQSLQPGISEDLKKVKDRMGIDSSDKVD  
FFILLDNVAAEQAHNLPSCPMLKRFARMIEQRAVDTSLYILPKEDRESLQMAVGPFHLIES  
NLLKAMDSATAPDKIRKLYLYAAHDVTFIPLLMTLGIFDHKWPPFAVDLTMELYQHLESKEW  
FVQLYYHGKEQVPRGCPDGLCP LDMLNAMS VYTLSPEKYHALCSQTQVM EVGNEE

**Signal sequence:**

amino acids 1-23

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 218-222

**Casein kinase II phosphorylation site.**

amino acids 87-91, 104-108, 320-324

**Tyrosine kinase phosphorylation site.**

amino acids 280-288

**N-myristoylation site.**

amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

**Amidation site.**

amino acids 216-220

**Leucine zipper pattern.**

amino acids 10-32

**Histidine acid phosphatases phosphohistidine signature.**

amino acids 50-65

## **FIGURE 53**

CTCCTCTAACATACTTGCAGCTAAACTAAATATTGCTGCTGGGGACCTCCTTAGCCT  
TAAATTCAGCTCATCACCTCACCTGCCTGGTCATGGCTCTGCTATTCTCCTTGATCCTT  
GCCATTGACCAGACCTGGATTCCTAGCGTCTCCATCTGGAGTGCAGCTGGGGCCT  
CCACCGCTGTGAAGGGCGGGTGGAGGTGGAACAGAAAGGCCAGTGGGGACCGTGTGATG  
ACGGCTGGGACATTAAGGACGTGGCTGTGTTGTGCCGGAGCTGGCTGTGGAGCTGCCAGC  
GGAACCCCTAGTGGTATTTGTATGAGCCACCAGCAGAAAAAGAGCAAAGGTCTCATCCA  
ATCAGTCAGTTGCACAGGAACAGAAGATACTGGCTCAGTGTGAGCAAGAAGAAGTTATG  
ATTGTTCACATGATGAAGATGCTGGGCATCGTGTGAGAACCCAGAGAGCTCTTCTCCCCA  
GTCCCAGAGGGTGTCAAGGCTGGTGACGCCCTGGCATTGCAAGGGACGCGTGGAAAGTGAA  
GCACCAAGAACAGTGGTATACCGTGTGCCAGACAGGCTGGAGCCTCCGGCCGCAAAGGTGG  
TGTGCCGGCAGCTGGATGTGGGAGGGCTGTACTGACTCAAAACGCTGCAACAAGCATGCC  
TATGCCGAAAACCCATCTGGCTGAGCCAGATGTCATGCTCAGGACGAGAACACCCTCA  
GGATTGCCCTCTGGCCTTGGGGAAAGAACACACCTGCAACCATGATGAAGACACGTGGTCG  
AATGTGAAGATCCCTTGACTTGAGACTAGTAGGAGGAGACAACCTCTGCTCTGGCGACTG  
GAGGTGCTGACAAGGGGTATGGGCTCTGTCTGTGATGACAACACTGGGAGAAAAGGAGGA  
CCAGGTGGTATGCAAGCAACTGGCTGTGGAAAGTCCCTCTCCCTCAGAGACCGGA  
AATGCTATGCCCTGGGGTTGGCCGCATCTGGCTGGATAATGTTCGTTGCTCAGGGAGGAG  
CAGTCCCTGGAGCAGTGCCAGCACAGATTTGGGGTTCACGACTGCACCCACCAGGAAGA  
TGTGGCTGTCATCTGCTCAGTGTAGGTGGCATCATCTAATCTGTTGAGTGCCTGAATAGAA  
GAAAAACACAGAAGAAGGGAGCATTACTGTCTACATGACTGCATGGATGAACACTGATCT  
TCTTCTGCCCTGGACTGGACTTATACTTGGTGCCCTGATTCTCAGGCCTTCAGAGTTGG  
ATCAGAACTTACAACATCAGGTCTAGTTCTCAGGCCATCAGACATAGTTGGAACACTACATCA  
CCACCTTCCTATGTCTCCACATTGCACACAGCAGATTCCAGCCTCCATAATTGTGTGTAT  
CAACTACTTAAATACATTCTCACACACACACACACACACACACACACACACACACACATA  
CACCAATTGTCCCTGTTCTCTGAAGAACTCTGACAAAATACAGATTTGGTACTGAAAGAGA  
TTCTAGAGGAACGGAATTAAAGGATAAATTCTGAATTGGTTATGGGTTCTGAAATTG  
GCTCTATAATCTAATTAGATATAAAATTCTGGTAACCTTATTACAATAATAAGATAGCAC  
TATGTGTTCAAA

## **FIGURE 54**

MALLFSLILAICTRPGLASPGVRLVGGHLRCEGRVEVEQKGQWGTVCDDGWDIKDVAVL  
RELGCGAASGTPSGILYEPPAEEKEQKVLIQSVSCTGTEDTLAQCEQEEVYDCSHDEDAGASC  
ENPESSFSPVPEGVRLADGPGHCKGRVEVKHQNQWYTVCQTGWSLRAAKVVCRQLGCGRAVL  
TQKRCNKHAYGRKPIWLSQMCSGREATLQDCPSGPWGKNTCNHDEDTWVECEDPFDLRLVG  
GDNLCGSRLEVLLHKGVWGSVCDDNWGEKEDQVVCKQLGCGKSLSPSFRDRKCYGPGVGRIVL  
DNVRCSGEEQSLEQCQHRFWGFHDCTHQEDVAVICSV

**Signal sequence:**

amino acids 1-15

**Casein kinase II phosphorylation site.**

amino acids 47-51, 97-101, 115-119, 209-213, 214-218, 234-238,  
267-271, 294-298, 316-320, 336-340

**N-myristoylation site.**

amino acids 29-35, 43-49, 66-72, 68-74, 72-78, 98-104, 137-143,  
180-186, 263-269, 286-292

**Amidation site.**

amino acids 196-200

**Speract receptor repeated domain signature.**

amino acids 29-67, 249-287

## **FIGURE 55**

ACTGCACTCGGTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGAC  
CCACCGCGTCCCGGGACCGTGGCGGACCGTGGCGGCTACCAGGAAGAGTCTGCCGAAG  
GTGAAGGCCATGGACTTCATCACCTCCACAGCCATCCTGCCCTGCTGTTGGCTGCCTGGG  
CGTCTTCGGCCTTTCCGGCTGCTGCAGTGGGTGCGCGGGAAAGGCCTACCTGCGGAATGCTG  
TGGTGGTGATCACAGGCCACCTCAGGGCTGGCAAAGAATGTGCAAAAGTCTTCTATGCT  
GCGGGTGCTAAACTGGTGCTCTGGCCGAATGGTGGGCCCTAGAACAGCTCATCAGAGA  
ACTTACCGCTCTCATGCCACCAAGGTGCAGACACACAAGCCTACTTGGTGACCTTCGACC  
TCACAGACTCTGGGCCATAGTTGCAGCAGCAGCTGAGATCCTGCAGTGCTTGGCTATGTC  
GACATACTTGTCAACAATGCTGGATCAGCTACCGTGGTACCATCATGGACACACCACAGTGG  
TGTGGACAAGAGGGTCATGGAGACAAACTACTTGGCCCAGTTGCTCTAACGAAAGCACTCC  
TGCCTCCATGATCAAGAGGAGGCAAGGCCACATTGTCGCCATCAGCAGCATCCAGGGCAAG  
ATGAGCATTCCCTTCGATCAGCATATGCAGCCTCCAAGCACGCAACCCAGGCTTCTTGA  
CTGTCGCGTGCAGATGAAACAGTATGAAATTGAGGTGACCGTCATCAGCCCCGGCTACA  
TCCACACCAACCTCTGTAAATGCCATCACCGCGGATGGATCTAGGTATGGAGTTATGGAC  
ACCACCCACAGCCCAGGGCGAAGCCCTGTGGAGGTGGCCAGGATGTTCTGCTGCTGTGGG  
GAAGAAGAAGAAAGATGTGATCCTGGCTGACTTACTGCCTTCCTGGCTGTTATCTCGAA  
CTCTGGCTCCTGGCTCTTCAGCCTCATGCCCTCCAGGGCCAGAAAAGAGCGGAAATCC  
AAGAACTCCTAGTACTCTGACCAGCCAGGGCAGAGAAGCAGCACTTTAGGCTTGC  
TTACTCTACAAGGGACAGTTGCATTGAGACTTAATGGAGATTGCTCACAAGTGGG  
AAAGACTGAAGAACACATCTCGTCAGATCTGCTGGCAGAGGACAATAAAAACGACAACA  
AGCTTCTCCAGGGTGAGGGAAACACTTAAGGAATAATGGAGCTGGGTTAACACT  
AAAAACTAGAAATAAACATCTCAAACAGTAAAAAAAAAAGGGCGCGACTCTAG  
AGTCGACCTGCAGAAGCTTGGCCGCCATGCCAACTTGTATTGCAGCTTATAATGGTTAC

## **FIGURE 56**

MDFITSTAILPLLFGCLGVFGLFRLLQWVRGKAYLRNAVVIITGATSGLGKEAKVFYAAGA  
KLVLCGRNGGALEELIRELTASHATKVQTHKPYLVTFDLTDGAI  
VAAAEEILQCFGYVDIL  
VNNAGISYRGTIMDTTVDVDKRVMETNYFGPVALTKALLPSMIKRQGHIVAISSIQGKMSI  
PFRSAYAASKHATQAFFDCLRAEMEQYEIEVTVISPGYIHTNLSVNAITADGSRYGVMDTTT  
AQGRSPVEVAQDVLAAVGKKKDVLADLLPSLAVYLRTLAPGLFFSLMASRARKERKSNS

**Signal sequence:**

amino acids 1-21

**Transmembrane domain:**

amino acids 104-120, 278-292

**N-glycosylation site.**

amino acids 228-232

**Glycosaminoglycan attachment site.**

amino acids 47-51

**Casein kinase II phosphorylation site.**

amino acids 135-139, 139-143, 253-257

**Tyrosine kinase phosphorylation site.**

amino acids 145-153, 146-153

**N-myristoylation site.**

amino acids 44-50, 105-111, 238-244, 242-248, 291-297

**Amidation site.**

amino acids 265-269

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 6-17

## **FIGURE 57**

## **FIGURE 58**

MKFLLDILLPLLIIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSK  
LVLWDINKHGLEETAAKCKGLGAKVHTFVVDCSNREDIYSSAKVKAEIGDVSILVNNAGVV  
YTSDFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTVASAAGHVSVPFLAYC  
SSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVVNRLMH  
GILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMKAQ

**Signal sequence:**

amino acids 1-19

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 30-34, 283-287

**Casein kinase II phosphorylation site.**

amino acids 52-56, 95-99, 198-202, 267-271

**N-myristoylation site.**

amino acids 43-49, 72-78, 122-128, 210-216

## **FIGURE 59**

CCACCGCGTCCGGGACCGTGGCTGACTAGTTCTAGATCGCGAGCGGCCGCCGGCTC  
AGGGAGGAGCACCGACTCGGCCGCACCTGAGAGATGGTGGTGCCATGTGGAAGGTGATTG  
TTTCGCTGGCTCTGTTGATGCCCTGGCCCTGTGATGGGCTGTTCGCTCCCTATAAGAAGT  
GTTTCCATGCCACCTAACGGAGACTCAGGACAGCCATTATTCTCACCCCTACATTGAAGC  
TGGGAAGATCCAAAAGGAAGAGAATTGAGTTGGTCGGCCCTTCCCAGGACTGAACATGA  
AGAGTTATGCCGGCTTCCTCACCGTGAATAAGACTTACAACAGCAACCTCTTCTGGTT  
TTCCCAGCTCAGATAACAGCCAGAACGATGCCAGTAGTTCTCTGGCTACAGGGTGGCCGG  
AGGTTCATCCATGTTGGACTCTTGTGGAACATGGGCCTATGTTGTCACAAGTAACATGA  
CCTTGCCTGACAGAGACTCCCTGGACCACAAACGCTCTCCATGCTTACATTGACAATCCA  
GTGGGCACAGGCTTCAGTTTACTGATGATAACCCACGGATATGCAGTCATGAGGACGATGT  
AGCACGGGATTATACAGTGCACTAATTCAAGTTTCCAGATATTCTGAATATAAAAAATA  
ATGACTTTATGTCACTGGGGAGTCTTATGCAGGGAAATATGTGCCAGCATTGCACACCTC  
ATCCATTCCCTCAACCCCTGTGAGAGAGGGTGAAGATCAACCTGAACCGAATTGCTATTGGAGA  
TGGATATTCTGATCCGAATCAATTATAGGGGCTATGCAGAATTCTGTACCAAATTGGCT  
TGTTGGATGAGAACAAAAAGTACTTCCAGAACAGTGCATGAATGCATAGAACACATC  
AGGAAGCAGAACTGGTTGAGGCCTTGAAATACTGGATAAAACTACTAGATGGCGACTAAC  
AAGTGATCCTCTTACTTCCAGAATGTTACAGGATGTAGTAATTACTATAACTTTTGCCT  
GCACCGAACCTGAGGATCAGCTTACTATGAAATTGTCACTCCAGAGGTGAGACAA  
GCCATCCACGTGGGAATCAGACTTTAATGATGAACTATAGTGAAGACTTGCAGAG  
AGATACAGTACAGTCAGTTAACCATGGTTAAGTGAATAATTATAAGGTTCTGA  
TCTACAATGCCAATGGACATCATCGTGGCAGCTGCCCTGACAGAGCGCTCCTGATGGC  
ATGGACTGGAAAGGATCCCAGGAATACAAGAACGGAGAAAAAGTTGGAAGATCTTAA  
ATCTGACAGTGAAGTGGCTGGTTACATCCGGCAAGCGGGTGACTCCATCAGGTAATTATTC  
GAGGTGGAGGACATATTTACCCATGACCAGCCTCTGAGAGCTTGACATGATTAATCGA  
TTCATTATGAAAAGGATGGATCCTTATGTTGGA**TAA**ACTACCTTCCAAAAGAGAACAT  
CAGAGGTTTCATTGCTGAAAAGAAAATGTAAGGAAACAGAAAATGTCATAGGAATAAAAAAA  
TTATCTTTCATATCTGCAAGATTTCATCAATAAAATTATCCTTGAAACAAGTGAGC  
TTTGTTTGGGGGAGATGTTACTACAAAATTACATGAGTACATGAGTAAGAATTACA  
TTATTAACCTAAAGGATGAAAGGTATGGATGATGTGACACTGAGACAAAGATGTATAAATGA  
AATTAGGGCTTGAATAGGAAGTTTAATTCTCTAAAGAGTAAGTGAAAAGTGCAGTTG  
TAACAAACAAAGCTGTAACATCTTCTGCCAATAACAGAAGTTGGCATGCCGTGAAGGT  
GTTGGAAATATTATGGATAAGAATAGCTCAATTATCCAAATAATGGATGAAGCTATAA  
TAGTTTGGGAAAAGATTCTCAAATGTATAAAGTCTTAGAACAAAAGAACATTCTTGAAATA  
AAAATATTATATAAAAGTAAAAAAAAAA

## **FIGURE 60**

MVGAMWKVIVSLVLLMPGPCDGLFRSLYRSVSMPKGDSQPLFLTPYIEAGKIQKGREL  
SVPFPGLNMKSYAGFLTVNKTYNSNLFFWFFPAQIQPEDAPVVLWLQGGPGGSSMFGLFVEH  
GPYVVTSNMTLDRDFPWTTLMSMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLYSALIQF  
FQIFPEYKNNDFYVTGESYAGKYVPAIAHLIHSILNPVREVKINLNGIAIGDGYSDPESIIGG  
YAEFLYQIGLLDEKQKKYFQKQCHECIEHIRKQNWFEEAFEILDKLLDGDLTSDPSYFQNVTG  
CSNYYNFLRCTEPEDQLYYVKFLSLPEVRQAIHVGNNQTFNDGTIVEKYLREDTVQSVKPWLT  
EIMNNYKVLIYNGQLDIIVAAALTERSLMGMDWKGSQEYKKAEKVWKIFKSDSEVAGYIRQ  
AGDFHQVIIRGGGHILPYDQPLRAFDMINRFIYGKGWDPYVG

**Signal sequence:**

amino acids 1-22

**N-glycosylation site.**

amino acids 81-85, 132-136, 307-311, 346-350

**Casein kinase II phosphorylation site.**

amino acids 134-138, 160-164, 240-244, 321-325, 334-338, 348-352,  
353-357, 424-428

**Tyrosine kinase phosphorylation site.**

amino acids 423-432

**N-myristoylation site.**

amino acids 22-28, 110-116, 156-162, 232-238

**Serine carboxypeptidases, serine active site.**

amino acids 200-208

**Crystallins beta and gamma 'Greek key' motif signature.**

amino acids 375-391

## **FIGURE 61**

CGAGGGCTTCCGGCTCCGAATGGCACATGTGGAATCCCAGTCTTGTGGCTACAACAT  
TTTCCCTTCCTAACAGTCTAACAGCTGTTAACAGCTAGTGATCAGGGGTTCTTCTT  
GCTGGAGAAGAAAGGGCTGAGGGCAGAGCAGGGCACTCTCACTCAGGGTGACCAGCTCCTTG  
CCTCTGTGGATAACAGAGCATGAGAAAGTGAAGAGATGCAGCGAGTGAGGTGATGGAAG  
TCTAAAATAGGAAGGAATTGTGTGCAATATCAGACTCTGGGAGCAGTTGACCTGGAGAGC  
CTGGGGAGGGCTGCTAACAGCTTCAAAAAACAGGAGCGACTTCACTGGCTGGGAT  
AAGACGTGCCGGTAGGATAGGAAGACTGGTTAGTCCTAACATCAAATTGACTGGCTGGG  
TGAACCTAACAGCCTTAACCTCTGGGAGATGAAAACGATGGCTTAAGGGCCAGAAA  
TAGAGATGTTGAAAATAAAATTAAAAAGCAAGTATTTATAGCATAAAGGCTAGA  
GACCAAAATAGATAACAGGATCCCTGAACATTCTAACAGAGGGAGAAAGTATGTTAAAATA  
GAAAAACCAAAATGCAGAAGGAGGAGACTCACAGAGCTAAACCAGGATGGGACCTGGGTC  
AGGCCAGCCTTTGCTCCTCCGGAAATTATTTGGTCTGACCACTCTGCCTTGTGTTT  
GCAGAATCATGTGAGGGCCAACCGGGGAAGGTGGAGCAGATGAGCACACACAGGAGCCGTCT  
CCTCACCGCCGCCCTCTCAGCATGGAACAGAGGCAGCCCTGGCCCCGGGCTGGAGGTGG  
ACAGCCGCTGTGGTCTGCTCAGTGGCTGGGTGCTGGCCCCCAGCAGCCGG  
ATGCCTCAGTCAGCACCTCACTCTGAGAATCGTACTGGACCTCAACCACCTGACCGT  
CCACCAAGGGACGGGGCGTCTATGTGGGGCCATCAACCGGGTCTATAAGCTGACAGGCA  
ACCTGACCATCCAGGTGGCTCATAACAGACAGGGCAGAAGAGGACAACAAGTCTGTTACCCG  
CCCCTCATCGTGCAGCCCTGCAGCGAAGTGTCTACCCCTACCAACAATGTCAACAAGCTGCT  
CATCATTGACTACTCTGAGAACCGCCTGCTGGCCTGTGGGAGCCTCTACCAGGGGTCTGCA  
AGCTGCTGCCGTGGATGACCTCTCATCCTGGAGCCATCCCACAAGAAGGAGCACTAC  
CTGTCCAGTGTCAACAAGACGGGACCATGTACGGGTGATTGTGCGCTCTGAGGGTGAGGA  
TGGCAAGCTCTTACCGCACGGCTGTGGATGGGAAGCAGGATTACTTCCGACCTGTCCA  
GCCGGAAGCTGCCCGAGACCCCTGAGTCCTCAGCCATGCTGACTATGAGCTACACAGCGAT  
TTTGTCTCCTCTCATCAAGATCCCTCAGACACCCCTGGCCCTGGTCTCCACTTTGACAT  
CTTCTACATCTACGGCTTGCTAGTGGGGCTTGTCTACTTCTCACTGTCCAGCCGAGA  
CCCCTGAGGGTGTGGCCATCAACTCCGCTGGAGACCTCTTACACCTCACGCATCGTGC  
CTCTGCAAGGATGACCCCAAGTCCACTCATACGTGTCCCTGCCCTGGCTGCACCCGGC  
CGGGGTGGAATACCGCCTCTGCAGGCTGCTACCTGGCCAAGCCTGGGACTCACTGGCC  
AGGCCTTCAATATCACCAGCCAGGACATGACTCTGCCCTGTGCGCTTCCATCCAAAGGGCAGAAG  
CAGTATCACCACCCGCCGATGACTCTGCCCTGTGCGCTTCCATCCAAAGGGCAGAAG  
GCAGATCAAGGAGCGCCTGCAGCCTGCTACCAGGGCGAGGGCAACCTGGAGCTCAACTGGC  
TGCTGGGAAGGACGTCCAGTGCACGAAGGCGCTGTCCCCATCGATGATAACTCTGTGGA  
CTGGACATCAACCAGCCCTGGAGGCTCAACTCCAGTGGAGGGCTGACCTGTACACCAC  
CAGCAGGGACCGCATGACCTCTGTGCCCTCTACGTTACAACGGCTACAGCGTGGTTTG  
TGGGACTAAGAGTGGCAAGCTGAAAAGGTAAGAGTCTATGAGTCAGATGCTCAATGCC  
ATTCACCTCCTCAGCAAAGAGTCCCTCTTGGAGGTAGCTATTGGTGGAGATTTAATATAG  
GCAACTTATTTCTGGGAACAAAGGTGAAATGGGAGGTAAAGAAGGGTTAATTGTG  
ACTTAGCTCTAGCTACTCCTCCAGCCATCAGTCATTGGGTATGTAAGGAATGCAAGCGTA  
TTCAATATTCCAAACTTAAGAAAAACTTAAGAAGGTACATCTGCAAAAGCAAA

## **FIGURE 62**

MGTLGQASLFAPPGNYFWSDHSALCFAESCEGQPGKVEQMSTHRSRLLTAAPLSMEQRQPWP  
RALEVDSRSVVLSSVVWVLLAPPAAGMPQFSTFHSENRDWTFNHLTvhQGTGAVYVGAINRV  
YKLTGNLTIQVAHKTGPEEDNKSRYPPLIVQPCSEVLTNNVNKLIIIDYSENRLLAGSL  
YQGVCKLLRLDDLFLILVEPSHKKEHYLSSVNKTGTMYGIVRSEGEGDKLFIGTAVDGKQDY  
FPTLSSRKLP RDPESSAMLDYELHSDFVSSLIKIPSDTLALVSHFDIFYIYGFASGGFVYFL  
TVQPETPEGVAINSAGDLFYTSRIVRLCKDDPKFHSYVSLPFGCTRAGVEYRLLQAAYLAKP  
GDSLAQAFNITSQDDVLFIAIFSKGQKQYHHPPDDSACAFPIRAINLQIKERLQSCYQGEQN  
LELNWLLGKDQCTKAPVPIDDNFCGLDINQPLGGSTPVEGLTLYTTSRDRMTSVASYVYNG  
YSVVFVGTKSGKLKKVRVYEFRCSNAIHLLSKESLLEGSYWWRFNYRQLYFLGEQR

**Signal sequence:**

amino acids 1-32

**Transmembrane domain:**

amino acids 71-87

**N-glycosylation site.**

amino acids 130-134, 145-149, 217-221, 381-385

**Casein kinase II phosphorylation site.**

amino acids 139-143, 229-233, 240-244, 291-295, 324-328, 383-387,  
384-388, 471-475, 481-485, 530-534

**N-myristoylation site.**

amino acids 220-226, 319-325, 353-359, 460-466, 503-509

## **FIGURE 63**

AGGCTCCCGCGCGCGGCTGAGTGGACTGGAGTGGAAACCGGGTCCCCCGCGTTAGAGAACACGCG**A**TGACCA  
CGTGGAGCCTCOGGCGGAGGCCGCCGCACGCTGGACTCTGCTGCTGGTCGTCTGGCTTCCCTGGTGCCTCC  
GCAGGCTGGACTGGAGCACCCCTGGTCCCTCTGCGGCTCCGCATCGACAGCTGGGCTGCAGGCCAAGGGCTGGA  
ACTTCATGCTGGAGGATTCCACCTTCTGGATCTCGGGGCTCCATCACTATTTCGTGTGCCAGGGAGTACT  
GGAGGGACCGCCCTGCTGAAGATGAAGGCCCTGCTGAACACCCTCACCACTATGTTCCGTGGAACCTGCATG  
AGCCAGAAAGAGGCAAATTGACTTCTCTGGGAACCTGGACCTGGAGGCCCTCGTCTGTGGCCAGAGATCG  
GGCTGTGGGTATTCTGCTCCAGGCCCTACATCTGCTGAGATGGACCTCGGGGCTGCCAGCTGGCTAC  
TCCAAGACCCCTGGCATGAGGCTGAGGACAACCTAACAGGGCTCACCGAACAGCTGGACCTTATTGACCACC  
TGATGTCCAGGGTGGTGCCTACTCCAGTACAAGCGTGGGGAGCTATCTGGCTGCAGGTGAGAAATGAATATG  
GTTCTATAATAAAGACCCCGCATACATGCCCTACGTCAAGAAGGACTGGAGGACCGTGGCATTGTGGAACCTGC  
TCCTGACTTCAGACAACAAGGATGGGTGAGCAAGGGATTGTCCAGGGAGTCTTGGCCACCATCAACTTGCAGT  
CAACACAGAGCTGCAGCTACTGACCACCTTCTCTTCAACGTCCAGGGACTCAGCCAAAGATGGTGTGGAGT  
ACTGGACGGGGTGGTTGACTCGTGGGAGGCCCTCACAAATATCTTGGATTCTCTGAGGTTTGAAAACCGTGT  
CTGCCATTGTGGACGCCGCTCCATCAACCTCTACATGTTCCACGGAGGCACCAACTTGGCTTCATGAATG  
GAGCCATGCACTCCATGACTACAAGTCAGATGTCACCAGCTATGACTATGATGCTGTGCTGACAGAACGGCG  
ATTACACGGCCAAGTACATGAAGCTTCGAGACTTCTCGGCTCCATCTCAGGCATCCCTCTCCCTCCCCACCTG  
ACCTTCTTCCAAGATGCCGTATGAGCCCTTAACGCCAGTCCTGTACCTGTCTGTGGACGCCCTCAAGTACC  
TGGGGAGCCAATCAAGTCTGAAAAGCCATCAACATGGAGAACCTGCCAGTCATGGGGAAATGGACAGTCCT  
TCGGGTACATTCTCTATGAGACCAGCATCACCTCGTCTGGCATCCTCAGTGGCCACGTGCATGATGGGGCAGG  
TGTTTGTGAACACAGTATCCATAGGATTCTGGACTACAAGACAACGAAGATTGCTGTCCCCCTGATCCAGGGTT  
ACACCGTGTGAGGATCTGGTGGAGAATCGTGGCGAGTCACATGGGGAGAATTGATGACCAGCGCAAAG  
GCTTAATTGGAAATCTCTATCTGAATGATTACCCCCTGAAAAACTTCAGAATCTATAGCCTGGATATGAAGAAGA  
GCTTCTTCAGAGGTTGGCCTGGACAAATGGNTTCCCTCCAGAAACACCCACATTACCTGCTTCTTCTTGG  
GTAGCTTGTCCATCAGCTCACGCCCTGTGACACCTTCTGAAGCTGGAGGGCTGGAGAAAGGGGTTGTATTCA  
TCAATGGCCAGAACCTTGGACGTTACTGGAACATTGGACCCAGAACAGCCTTACCTCCAGGTCCCTGGTTGA  
GCAGCGGAATCAACCAGGTATCGTTTGAGGAGACGATGGGGCCCTGCATTACAGTTACGGAAACCCCCC  
ACCTGGGAGGAACCACTGATGGCTGGCACCCTCTGCTGGTGCAGTGGGAGACTGCCGCC  
CTCTTGACCTGAACCTGGCTGCTGGCCACCCCTCAGTCAAAAGCATCTCTTAAAGTAGCAACCTCAGGG  
ACTGGGGCTACAGTCTGCCCCCTGCTCAGTCAGTCAAAACCCCTAAGCCTGCAGGGAAAGGTGGATGGCTCTGGGCC  
TGGTTTGTGATGGCTTCTCACAGCCCTGCTCTTGTGCGGAGGCTGTGGGCTGTCTAGGGTGGAGC  
AGCTAATCAGATGCCAGCCTTGGCCCTCAGAAAAAGTGTGAAACGTGCCCTGCACCGGACGTACAGCCC  
TGCAGCATCTGCTGGACTCAGCGTGCTCTTGTGCTGGCTCTGGGAGGCTGGCCACATCCCTCATGGCCCC  
TTTATCCCCGAATCCTGGGTGTGTCACAGTGTAGAGGGTGGGAAGGGGTGTCTCACCTGAGCTGACTTGT  
CTTCCTTCACAACCTCTGAGCCTCTTGGATTCTGAAGGAACCTGGCGTGAAGAACATGTGACTTCCCC  
TCCCTCCCACTCGCTGCTTCCCACAGGGTGACAGGCTGGAGAAACAGAAATCCCTCACCTGCGTCTTCC  
CAAGTTAGCAGGTGTCTGGTGTGTCAGTGAGGAGGACATGTGAGTCTGGCAGAACGCCATGCCCATGTCTGCA  
CATCCAGGGAGGAGGACAGAACGGCCAGCTCACATGTGAGTCTGGCAGAACGCCATGCCCATGTCTGCAACATCC  
AGGGAGGAGGACAGAACGGCCAGCTCACATGTGAGTCTGGCAGAACGCCATGCCCATGTCTGCAACATCCAGGG  
GGAGGACAGAACGGCCAGCTCACATGTGAGTCTGGCAGAACGCCATGCCCATGTCTGCAACATCCAGGGAGG  
ACAGAACGGCCAGCTCAGTGGCCCCGCTCCCCACCCCCCAGGCCAACAGCAGGGCAGAGCAGCCCTCC  
GAAGTGTGTCAGTCCGATTTGAGCCTTGTCTGGGCCCCAGCCAAACACCTGGCTTGGCTACTGCTCTGA  
GTTGCAGTAAAGCTATAACCTTGAATCACAA

## **FIGURE 64**

MTTWSLRRR PARTLGLLLLVVLGFLVLRRLDWSTLVPLRLRHQLGLQAKGWNFMLEDSTFW  
IFGGSIHYFRVPREYWRDRLLKMKACGLNTLTTYVPWNLHEPERGKFDFSGNLDLEAFVLMA  
AEIGLWVILRPGPYICSEMDLGGLPSWLLQDPGMRLRTTYKGFTEAVIDLYFDHLMMSRVVPLQ  
YKRGGPIIAVQVENEYGSYNKDPAYMPYVKKALEDRGIVELLTSNDKDGLSKGIVQGVLAT  
INLQSTHELQLLTTFLNVQGTQPKMVMEYWTGFDSWGGPHNILDSSEVLKTVSAIVDAGS  
SINLYMFHGGTNFGFMNGAMHFHDYKSDVTSYDYDAVLTEAGDYTAKYMKLRDFFGSISGIP  
LPPPPDLPKMPYEPLTPVLYLSLWDALKYLGEPIKSEKPINMENLPVNGGNGQSFYIYE  
TSITSSGILSGHVHDRGQVFVNTVSIGFLDYKTTKIAVPLIQGYTVLRILVENRGRVNYGEN  
IDDQRKGLIGNLYLNDSPLKNFRIYSLDMKKSFFQRFGLDKWXSLPETPTLPAFFLGSLIS  
STPCDTFLKLEGWEKVVFINQNLGRYWNIGPQKTLYLPGPWLSSGINQVIVFEETMAGPA  
LQFTETPHLGRNQYIK

**Signal sequence:**

amino acids 1-27

**Casein kinase II phosphorylation site.**

amino acids 141-118, 253-257, 340-344, 395-399, 540-544, 560-564

**N-myristoylation site.**

amino acids 146-152, 236-242, 240-246, 244-250, 287-293, 309-315,  
320-326, 366-372, 423-429, 425-431, 441-447, 503-509, 580-586

## FIGURE 65

GGGGACGGGAGCTGAGAGGCTCCGGCTAGCTAGGTGTAGGGTGGACGGTCCCAGGACC  
CTGGTGAGGGTCTCTACTTGGCCTCGGTGGGGTCAAGACGCAGGCACCTACGCCAAAGG  
GGAGCAAAGCCGGCTCGGCCGAGGCCCGAGGACCTCATCTCCAATGTTGGAGGAATC  
CGACACGTGACGGTCTGTCGCCGTCTCAGACTAGAGGAGCGCTGAAACGCCATGGCTCC  
AAGAAGCTGTCCTGCCTCGTCCCTGCTGCTGCCGCTCAGCCTGACGCTACTGCTGCCCA  
GGCAGACACTCGTCGTTGCTAGGGATAGGGGTATGACCGGTTCTCCTAGACGGGCC  
CGTTCGCTATGTGTCGGCAGCCTGCACTACTTCGGGTACCGCGGGTGCTTGGGCCAC  
CGGCTTTGAAGATGCGATGGAGCGGCCTCAACGCCATACAGTTATGTCGCCCTGGAAC  
CCACGAGCCACAGCCTGGGGTCTATAACTTAATGGCAGCCGGACCTCATGCCCTTCTGA  
ATGAGGCAGCTCTAGCGAACCTGTTGGTCATACTGAGACCAAGGACCTACATCTGTGCAGAG  
TGGGAGATGGGGGTCTCCCATCCTGGTTGCTCGAAAACCTGAAATTCACTTAAGAACCTC  
AGATCCAGACTCCTGCGCAGTGGACTCCTGGTTCAAGGTCTGCTGCCAAGATATATC  
CATGGCTTATCACAAATGGGGCAACATCATTAGCATTAGGTGGAGAATGAATATGGTAGC  
TACAGAGCCTGTGACTTCAGCTACATGAGGCACCTGGCTGGCTCTCGTGCACGTCTAGG  
AGAAAAGATCTGCTCTCACACAGATGGGCCTGAAGGACTCAAGTGTGGCTCCCTCCGGG  
GAECTATACCACTGTAGATTGGCCAGCTGACAACATGACCAAAATCTTACCCCTGCTT  
CGGAAGTATGAACCCCATGGGCATTGGTAAACTCTGAGTACTACACAGGCTGGCTGGATTA  
CTGGGGCCAGAATCACTCCACACGGTCTGTGTCAGCTGTAACCAAGGACTAGAGAACATGC  
TCAAGTTGGGAGCCAGTGTGACATGTACATGTTCCATGGAGGTACCAACTTGGATATTGG  
AATGGTGCCGATAAGAAGGGACGCTCCCTCGATTACTACCAGCTATGACTATGATGCACC  
TATATCTGAAGCAGGGGACCCACACCTAACGCTTTGCTCTCGAGATGTACAGCAAGT  
TCCAGGAAGTCCCTTGGGACCTTACCTCCCCGAGCCCCAAGATGATGCTGGACCTGTG  
ACTCTGCACCTGGTTGGCATTACTGGCTTCTAGACTTGTGCTTGGCCCCGTGGGCCAT  
TCATTCAATCTGCCAATGACCTTGAGGCTGTCAGCAGGACATGGCTCATGTTGTACC  
GAACCTATATGACCCATACCATTGGAGCCAACACCATTCTGGGTGCCAATAATGGAGTC  
CATGACCGTGCCATGTGATGGTGGATGGGTGTTCCAGGGTGTGGAGCGAAATATGAG  
AGACAAACTATTTTGACGGGAAACTGGGTCAAACCTGGATATCTGGTGGAGAACATGG  
GGAGGCTCAGCTTGGGTCTAACAGCAGTGACTCAAGGGCCTGTTGAAGCCACCAATTCTG  
GGGCAAACAATCCTAACCACTGGATGATGTTCCCTGAAAATTGATAACCTGTGAAGTG  
GTGGTTCCCTCCAGTTGCCAAATGCCATATCCTCAAGCTCCTCTGGCCCCACATTCT  
ACTCCAAAACATTCCAATTAGGCTCAGTTGGGACACATTCTATATCTACCTGGATGG  
ACCAAGGGCAAGTCTGGATCAATGGGTTAACCTGGGCCGGTACTGGACAAAGCAGGGCC  
ACAACAGACCCCTACGTGCCAAGATTCTGCTGTTCTAGGGAGCCCTAACAAAATTA  
CATTGCTGGAACCTAGAAGATGTACCTCTCCAGCCCCAAGTCCAATTGGATAAGCCTATC  
CTCAATAGCACTAGTACTTGCACAGGACACATATCAATTCCCTTCAGCTGATAACTGAG  
TGCCTCTGAACCAATGGAGTTAAGTGGCACTTGAAAGGTAGGCCGGCATGGTGGCTCATGC  
CTGTAATCCCAGCACTTGGGAGGCTGAGACGGGTGGATTACCTGAGGTCAAGGACTTCAAGA  
CCAGCCTGGCCAACATGGAAACCCCGTCCACTAAAAAATACAAAATTAGCCGGCGTG  
ATGGTGGGCACCTCTAATCCCAGCTACTGGGAGGCTGAGGGCAGGAGAATTGCTTGAATCC  
AGGAGGCAGAGGTTGCAGTGAGTGGAGGTTGTACCACTGCACTCCAGCCTGGCTGACAGTGA  
GACACTCCATCTCAAAAAAAAAAA

## **FIGURE 66**

MAPKKLSCLRSLLLPLSLTLLPQADTRSFVVDRGHDRFLLDGAPFRYVSGSLHYFRVPRVL  
WADRLLKMRWSGLNAIQFYVPWNYHEPQPGVNFNGSRDLIAFLNEAALANLLVILRPGPYI  
CAEWEMGGPSWLLRKPEIHLRTSDPDFLAAVDSWFKVLLPKIYPWLYHNGGNIISIQVENE  
YGSYRACDFSYMRHLAGLFALLGEKILLFTTDGPEGLKCGSLRGGLYTTVDFGPADNMTKIF  
TLLRKYEPhGPLVNSEYYTGWLWQNHSTRSAVTKGLENMLKLGASVNMYMFHGKTNF  
GYWNGADKKGRFLPITTSYDYDAPISEAGDPTPKLFALRDVISKFQEVPGLPLPPSPKMML  
GPVTLHLVGHLLAFLDLLCPRGPIHSILPMTFEAVKQDHGFMLYRTYMTHTIFEPTPFWVPN  
NGVHDRAYVMVDGVFQGVVERNMRDKLFLTGKLGSKLDILVENMGRLSFGSNSSDFKGLLKP  
PILGQTILTQWMMFPLKIDNLVWWFPLQLPKWPYPQAPSGPTFYSKTFPILGSVGDTFLYL  
PGWTKGQVWINGFNLGRYWTQGPQQTLYVPRFLFPRGALNKITLLELEDVPLQPQVQFLD  
KPILNSTSTLHRTHINSLSADTLSASEPMELSGH

**Signal sequence:**

amino acids 1-27

**N-glycosylation site.**

amino acids 97-101, 243-247, 276-280, 486-490, 625-629

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 4-8

**Casein kinase II phosphorylation site.**

amino acids 148-152, 234-238, 327-331, 423-427, 469-473, 550-554,  
603-607, 644-648

**Tyrosine kinase phosphorylation site.**

amino acids 191-198

**N-myristoylation site.**

amino acids 131-137, 176-182, 188-194, 203-209, 223-229, 227-233,  
231-237, 274-280, 296-300, 307-313, 447-453, 484-490

## **FIGURE 67**

GCTTGAAACACGTCTGCAAGCCAAAGTTGAGCATCTGATTGGTTATGAGGTATTCAGTGC  
ACCCACAATATGGCTTACATGTTAAAAAGCTTCTCATCAGTTACATATCCATTATTGTGT  
TTATGGCTTATCTGCCCTACACTCTCTCTGTTATTCAAGGATAACCTTGAAGGAATATT  
CTTCGAAAAGTCAGAGAAGAGAGCAGTTAGTGCACATTCCAGATGTCAAAACGATT  
GCGTCCTTCTCACATGGTAGACCAGTATGACCAGCTATATTCCAAGCGTTGGTGTGTT  
CTTGTCAAGAGTTAGTGAAGAAATAACTAGGGAAATTAGTTGAACCATGAGTGGACATTG  
AAAAACTCAGGCAGCACATTCAACGCAACGCCAGGACAAGCAGGAGTTGCATCTGTTCATG  
CTGTCGGGGTGCCCAGTGTGCTTGACCTCACAGACCTGGATGTGCTAAAGCTTGAAC  
AATTCCAGAAGCTAAATTCTGCTAACAGATTCTCAAATGACTAACCTCAAGAGCTCCACC  
TCTGCCACTGCCCTGCAAAAGTTGAACAGACTGCTTTAGCTTCTCGCGATCACTGAGA  
TGCCTTCACGTGAAGTTCACTGATGTGGCTGAAATTCTGCCTGGGTGTATTGCTAAAAAA  
CCTTCGAGAGTTGTACTTAATAGGCAATTGAACACTCTGAAAACAATAAGATGATAGGACTTG  
AATCTCTCCGAGAGTTGGCACCTTAAGATTCTCACGTGAAGAGCAATTGACCAAAGTT  
CCCTCCAACATTACAGATGTGGCTCCACATCTTACAAAGTTAGTCATTATAATGACGGCAC  
TAAACTCTGGTACTGAACAGCCTTAAGAAAATGATGAATGTCGCTGAGCTGGAACTCCAGA  
ACTGTGAGCTAGAGAGAATCCCACATGCTATTTCAGCCTCTCTAACAGGAACTGGAT  
TTAAAGTCAAATAACATTGCAACATTGAGGAAATCATCAGTTCCAGCATTAAAACGACT  
GACTTGTAAAATTATGGATAACAAAATTGTTACTATTCCCTCCCTATTACCCATGTCA  
AAAACCTGGAGTCACTTATTCTCTAACACAAGCTCGAACCTTACAGTGGCAGTATT  
AGTTACAGAAACTCAGATGCTTAGATGTGAGCTACAACAACATTCAATGATTCAATAGA  
AATAGGATTGCTTCAGAACCTGCAGCATTTGCATATCACTGGAACAAAGTGGACATTCTGC  
CAAACAAATTGTTAAATGCATAAAGTTGAGGACTTGAATCTGGACAGAACTGCATCACC  
TCACTCCCAGAGAAAGTTGGTCAGCTCTCCAGCTCACTCAGCTGGAGCTGAAGGGAACTG  
CTTGGACCGCCTGCCAGCCCAGCTGGCCAGTGTGGATGCTCAAGAAAAGCGGGCTGTTG  
TGGAGATCACCTTTGCAAATGGATTAAAACTAAGATAATATGACACAGTGTGCAGGAAC  
AACTCCTAGATTGCAAGTGCTCACGTACAAGTTATTACAAGATAATGCATTAGGAGTAG  
ATACATCTTTAAAATAACAGAGAGGATGCATAGAAGGCTGATAGAAGACATAACTGAAT  
GTTCAATGTTGTAGGGTTAAAGTCATTCACTTCAAATCATTGTTTTCTTTGGGG  
AAAGGGAAGGAAAATTATAATCACTAATCTGGTTCTTTAAATTGTTGTAACCTGGAT  
GCTGCCGCTACTGAATGTTACAAATTGCTGCCTGCTAAAGTAAATGATTAAATTGACATT  
TTCTTACTAAAAAAAAAAAAAA

## **FIGURE 68**

MAYMLKKLLISYISIICVYGFICLYTLFWLFRIPLKEYSFEKVREESSFSDIPDVKNDFAFL  
LHMVDQYDQLYSKRGVFLSEVSENKLREISLNHEWTFEKLRQHISRNAQDKQELHLFMLSG  
VPDAVFDLTDLDVLKLELIPEAKIPAKISQMNTNLQELHLCHCPAKVEQTAFSFLRDHLRCLH  
VKFTDVAEIPAWVYLLKNLRELYLIGNLNSENNKMIGLESLRELRLKILHVKSNLTKVPSN  
ITDVAPHLTKLVIHNDGTKLLVLNSLKKMMNVAELELQNCELERIPHAIFSLSNLQELDLKS  
NNIRTIEIIISFQHLKRLTCLKLWHNKIVTISSITHVKNLESLYFSNNKLESLPVAVFSLQ  
KLRCLDVSYNNISMIPIEIGLLQNLQHLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLP  
EKVGQLSQLTQLELKGNCLDRPAQLGQCRMLKKSGLVVEDHLFDTLPLEVKEALNQDINIP  
FANGI

**Signal sequence:**

amino acids 1-20

**N-glycosylation site.**

amino acids 241-245, 248-252, 383-387

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 326-330

**Casein kinase II phosphorylation site.**

amino acids 48-52, 133-137, 226-230, 315-319, 432-436, 444-448

**Tyrosine kinase phosphorylation site.**

amino acids 349-355, 375-381

**N-myristoylation site.**

amino acids 78-84, 124-130, 212-218, 392-398

## **FIGURE 69**

CC CAC CG CG TCC GGC CT TCT CT GG ACT TT GC ATT CC ATT TTT CATT GA CA AA ACT GA CT TTT TATT TCT  
TTT TT CC AT CT CT GG CC AG CT GG AT CC TAGG CG CC CT GG AAG AC AT TT GT GT TT AC AC AC TA AGG AT  
CT GT GT TT GG GG TT CT TCT CC CT GG AC AT TT GG CATT GC AT TG CT TAG GT GT GT GG GG AG AC AC GT GG  
GT CAG TG CT TG CT TG CACT TAT CT GC CT AGG TA CAT CG AAGT CTT TGA CCT CC AT AC AGT GATT AT GC CT GT C  
AT CG CT GG GT AT CT GG CC CT TG CT CT GT CAG TG AT GT GT GT CT GT CT GT CT TTA CT TCA AA AT AC AC AA  
GC GCT AAA AG CT GCAA AGG AACC TG AAG CT GT GG CT GT AAAA AT CA AC CC AG AC AAG GT GT GG GT GG CC AAG  
AAC AG CC AGG CCAA ACC AT TG CC AC GG AG TG CT GT CT GG CC TG CAG TG CT GT GAA AGG AT AT AGA AT GT GT GCC  
AG TTT GAT TCC TG CC AC CT TG CT GT TG CG AC AT AA AT GAG GG CT TG AG GT TAG GAA AGG CT CC CT TCT CAAA  
GC AG AG CC CT GA AG AC TT CA AT GT CA AT GAG GG CC AC CT GT TT GT GAT GT GC AGG CAC AG AAG GAA AGG CAC AG  
CT CCC AT CAG TT CAT GG AAA AT AAT CAG TG CT GG AACC AG CT GT GG AG AT CC CT AC AG AG AG CT TC  
CA CT GG GG CA ACC CT TG CAGG AAGG AG TG GT GG AG AG AACC CT AC TG GT GG AAT GT GATA AAC CAGT CA  
CAC AG TG CT CT ATT CT CA CAA AT CT ACC C CT TG CT TG CT GG ACT GAC GT TT CC TG AG GT GT CC AG AAA  
GCT GAT GT A AC AC AG AG CC TATA AA AG CT GT CG TG CCT TA AGG CT GG CC AG CG CC TT TG CCAA AT GG AG CT TG TA  
AGA AGG CT CAT GG CATT GAC CC CT TT AATT CT CT CT GT TT GG CG GAG CT GACA AT GG CG AGG CT GA AGG CA AT  
GCA AG CT GC AC AG T CAG T CT AGGG GT GG CA AT AT GG CAG AG ACC CAA AG CC AT GAT CT GCA AT CT CA AT CCC  
AGT GAG AACT GCA CCT GG AC AAT AG AAG ACC AG AAAA AC AA AGC AT CAG AATT AT CT TT CT AT GT CAG CTT  
GAT CC AG AT GG AAG CT GT GAA AGT GAAA AC AT AA AGT CTT GAC GG AA CCT CC AG CAA TGG C CT TG CT AGGG  
CA AGT CT G CAG TAAA AC GACT AT GT CT CT GT ATT TG AAT CAT C AT CC CAG T AC ATT GAC GT TT CAA AT AGT TACT  
GA CT CAG CA AG AATT CAA AG AACT GT CT TT GT CT TACT AC TT CT CT CTA AC AT CT CT AT TT CAA ACT GT  
GG CG GT TAC CT GG AT AC CT TG GA AGG AT CCT TG CACC AG CCCC AT TA CCAA AG CC GCA T CT TG AG CT GG CT TAT  
TGT GT GT GG CAC AT ACA AGT GG AGA AAG ATT ACA AG AATA ACT AA ACT CAA AG AG AT TT CT AG AAT AG AC  
AA AC AGT G CAA AT TT GAT TT CT GG C AT CT AT GAT GG CC CT CC ACC AACT CT GG CT GAT GG AC AGT CT GT  
GG CG GT GACT CCC AC CT TG AAT CGT C AT CAA ACT CT CT GACT GT CG TG TT GT CT AC AG AAT AT GCA AT TT CT  
TAC CG GG GAT TT CT GCT TCT AC AC CT CA ATT TAT G CAG AAA AC AT CA AC ACT AC AT CT TA ACT TG CT CT  
GAC AGG AT GAG GT TATT ATA AG CAA AT CCT AC CT AGG GCT TT TA ACT CT AAT GGG AATA ACT TG CAA CT AAAA  
GAC CCA ACT TG CAG AG CAA AATT AT CAA AT GT GT GG AATT TT CT GT CC CT TA AT GG AT GT GG TAC AAT CAG A  
AAG GT AGA AG AT CAG T CAA ATT ACT TG CAC CA AAT AT CAC CT TT CT G C AT CCT CA ACT TT CT G AAG T GAT C ACC  
CG T CAG A A A C A C T C C CAG AT T AT GT G AAG T GT G AAT GG G A C A T A T C A T C A G T G G A G A T A A T A C A T A A C A  
GA AG AT GAT GT A AT ACA AA AGT CAA AA G C A C T G G G C A A A T A A C A C C A G C A T G G C T C T T T G A A T C C A A T T C A  
TT GAAA AG ACT A T A C T T G A A T C A C C A T A T T A T G T G A T T G A A C C A A C T C T T T G T T C A A G T T A G T C T G C A C  
AC CT CAG AT C C A A A T T T G G T G G T T C T T G A T A C C T G T A G A G C C T C T C C C A C C T G A C T T T G C A T C T C C A A C C  
TAC GAC CT A AT CA A C A G A G T G G A T G T A G T C G A G A T G A A A C T T G T A A G G T G T A T C C T T A T T T G G A C A C T A T G G G A G A  
TT CC AG T T A T G C C T T A A T T C T G A G A A G T A T G G C T C T G T G A T C T G C A G T G T A A G T T T G A T A T G T G A T  
AG CAG TG ACC ACC AG T C T C G C T G C A A T C A A G G T T G T G T C C A G A A G C A A A C G A G A C A T T T C T T C A T A T A A T G G  
AAA AC AG A T T C C A T C A T G G A C C C A T T C G T C T G A A A A G G G A T C G A A G T G C A A G T G G C A A T T C A G G A T T T C A G C A T  
GAA AC AC AT G C G G A A G A A A C T C C A A A C C A G C C T T C A A C A G T G T G C A T C T G T T T C C T T C A T G G T T C T A G C T C G  
AAT GT GGT GACT GT AG CG A C A T C A C A G T G A G G C A T T T G T A A A T C A A C G G G C A G A C T A C A A A T A C C A G A A G C T G  
CAG A A C T A T T A A C T A A C A G G T C C A A C C T A A G T G A G A C A T G T T C T C C A G G A T G C C A A A G G A A T G C T A C C T C G T  
GG C T A C A C A T A T T A T G A A T A A T G A G G A A G G G C C T G A A A G T G A C A C A C A G G C C T G A T G T A A A A A A A A

## **FIGURE 70**

MELVRRLMPLTLLLILSCLAEALTMAEAEGNASCTVSLGGANMAETHKAMILQLNPSENCTWTI  
ERPENKSIRIIFSYVQLDPDGSCESENIKVFDGTSSNGPLLQVC SKNDYVPVFESSSTLT  
FQIVTDSARIQRTVFVFFSPNISIPNCGGYLDTLEGSFTSPNYPKPHPELAYCVWHIQV  
EKDYKIKLNFKEIFLEIDKQCKFDLAIYDGPSTNSGLIGQVCGRVPTFESSNSLTVVLS  
TDYANSYRGFSASYTSIYAENINTTSLTCSSDRMVIISKSYLEAFNSNGNNLQLKDPTCRP  
KLSNVVEFSVPLNGCGTIRKVEDQSITYTNIIITFSASSTSEVITRQKQLQIIVKCEMGHNST  
VEIIYITEDDVIQSQNALGKYNTSMALFESNSFEKTILESPYYVDLNQTLFVQVSLHTSDPN  
LVVFLDTCRASPTSDFASPTYDLIKSGCSRDETCKVYPLFGHYGRFQFNFKFLRSMSSVYL  
QCKVLICDSSDHQSRCNQGCVSRSKRDIISSYWKTDSSIIGPIRLKRDRSASGNQFHETHA  
EETPNQPFNSVHLFSFMVLALNVVTVATITVRHFVNQRADYKYQKLQNY

**Signal sequence:**

amino acids 1-24

**Transmembrane domain:**

amino acids 571-586

**N-glycosylation site.**

amino acids 29-33, 57-61, 67-71, 148-152, 271-275, 370-374,  
394-398, 419-423

**Casein kinase II phosphorylation site.**

amino acids 22-26, 108-112, 289-293, 348-352, 371-375, 379-383,  
408-412, 463-467, 520-524, 556-560

**Tyrosine kinase phosphorylation site.**

amino acids 172-180, 407-415, 407-416, 519-528

**N-myristoylation site.**

amino acids 28-34, 38-44, 83-89, 95-101, 104-110, 226-232

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18

## **FIGURE 71**

GACGGAAGAACAGCGCTCCCGAGGCCGCGGGAGCCTGCAGAGAGGACAGCCGGCTGCGCCG  
GGACATGCGGCCCCAGGAGCTCCCAGGCTCGCGTTCCCGTTGCTGCTGTTGCTGC  
TGCTGCGCCGCCGCGTGCCTGCCACAGGCCACGCCCTCGACCCCCACTGGGAGTCC  
CTGGACGCCGCCAGCTGCCCGTGGTTGACCAAGGCCAGTCGGTAGCGAGTGGTTCTGGTGGATTGGAAAAGGAAA  
AGATACCGAAGTATGTGAAATTATGAAAGATAATTACCCCTAGTTCAAATATGAAGAT  
TTTGGACCACATTACAGCAAATTTTAATGCCAACAGTGGCAGATATTTCAAGGC  
CTCTGGTGC<sub>AA</sub>AATACATTGCTTAACCTCCAAACATCATGAAGGCTTACCTGTGGGGT  
CAGAATATTGCGGAACTGGAATGCCATAGATGAGGGGCCAAGAGGGACATTGTCAAGGAA  
CTTGAGGTAGCCATTAGGAACAGAACTGACCTGCGTTGGACTGTACTATTCCCTTTGA  
ATGGTTTCA<sub>TCG</sub>CTTCC<sub>CT</sub>TGAGGATGAATCAGTCATTCCATAAGCGGCAATTCCAG  
TTTCTAAGACATTGCCAGAGCTCTATGAGTTAGTGAACA<sub>ACT</sub>TACAGCCTGAGGTTCTGTGG  
TCGGATGGTGACGGAGGAGCACCGGATCAAA<sub>ACT</sub>TGGAACAGCACAGGCTTCTGGCCTGGTT  
ATATAATGAAAGCCCAGTCGGGGCACAGTAGTCACCAATGATCGTTGGGAGCTGGTAGCA  
TCTGTAAGCATGGTGGCTTCTACCTGCAGTGATCGTTATAACCCAGGACATCTTGC<sub>CA</sub>  
CATAAATGGAAA<sub>ACT</sub>GCAATAGACAA<sub>ACT</sub>GTCCTGGGCTATAGGAGGGAA<sub>AGCT</sub>GG  
AA<sub>AT</sub>CTGACTATCTACAATTGAAGAATTGGTGAAGCAACTTG<sub>TA</sub>GAGACAGTTCATGTG  
GAGGAAATCTTGATGAATATTGGGCCACACTAGATGGCACCA<sub>TT</sub>CTGTAGTTTGAG  
GAGCGACTGAGGCAAGTGGGCTGGCTAAAGTCATGGAGAAGCTATTATGAAACCTA  
TACCTGGCGATCCCAGAATGACACTGT<sub>C</sub>ACCCAGATGTGTGGTACACATCCAAGCCTAAAG  
AAAAATTAGTCTATGCCATT<sub>TT</sub>CTTAA<sub>AT</sub>GGCCCACATCAGGACAGCTGTTCTGGCCAT  
CCCAAGCTATTCTGGGGCAACAGAGGTGAA<sub>ACT</sub>ACTGGGCCATGGACAGCCACTTA<sub>ACT</sub>GT  
GATTCTTGAGCAAA<sub>AT</sub>GGCATTATGGT<sub>AG</sub>ACTGCCACAGCTAACCATTCAGATGC  
CGTGTAA<sub>AT</sub>GGGCTGGCTCTAGCC<sub>TA</sub>ACTAATGTGATCTAAAGTGCAGCAGAGTGGCTG  
ATGCTGCAAGTTATGTCTAAGGCTAGGA<sub>ACT</sub>TACAGGTGTCTATAATTG<sub>TAG</sub>GCACATGGAGA  
AAGCAATGTA<sub>AA</sub>ACTGGATAAGAAAATTATTGGCAGTTCA<sub>G</sub>CCCTTCC<sub>TT</sub>CCACTA  
AATT<sub>TT</sub>CTTAA<sub>ATT</sub>ACCCATGTAACC<sub>TT</sub>TA<sub>CT</sub>CTCCAGTGCACTTG<sub>CC</sub>ATTAAAGTC  
TCTTCACATTGATTGTTCCATGTGTGACTCAGAGGTGAGAATT<sub>TT</sub>TCACATTATAGTAG  
CAAGGAATTGGTGGTATTATG<sub>AC</sub>CGA<sub>CT</sub>GTGAA<sub>ACT</sub>GAAAATT<sub>TT</sub>TATGTTGAAGCCATATCCCCCATG  
ATTATATAGTTATGCATCACTTAATATGGGATATTCTGGAA<sub>AT</sub>GCATTGCTAGTCAT  
TTTTTTTG<sub>GC</sub>CAACATCATAGAGTGTATT<sub>AC</sub>AA<sub>AT</sub>C<sub>CT</sub>AGATGGCATAGCCTACTACA  
CACCTAATGTGTATGGTATAGACTGTTGCTC<sub>CT</sub>AGGCTACAGACATATACAGCATGTTACTG  
AATACTGTAGGCAATAGTAACAGTGGTATTGTATATCGAAACATATGGAAACATAGAGAAG  
GTACAGTAAA<sub>AA</sub>ACTGTAAA<sub>AA</sub>ATGGTGCACCTGTATAGGGCACTTAC<sub>CA</sub>CGAATGGAG  
CTTACAGGACTGGAAGTTGCTCGGGTGAGTCAGTGAGTGAATGTGAAGGCCTAGGACATTA  
TTGAACACTGCCAGACGTTATAA<sub>AA</sub>ACTGTATGCTTAGGCTACACTACATTATAA<sub>AAAAAA</sub>  
GTTTTCTTCTCAATTATAA<sub>AA</sub>ACATAAGTGTACTGTA<sub>ACT</sub>TTACAAACGTTAATT  
TTTAAACCTTTGGCTTTGTAATAACACTAGCTAAACATAACTCATTGTGCAA  
ATGTA

## **FIGURE 72**

MRPQELPRLAFPLLLLLLPPPCPAHSATRFDPTWESLDARQLPAWFDQAKFGIFIFIHWG  
VFSVPSFGSEWFWWYWKKEKIPKYVEFMKDNYPPSFKYEDFGPLFTAKFFNANQWADIFQAS  
GAKYIVLTSKHHEGFTLWGSEYSWNWNAIDEGPKRDIVKELEVAIRNRTDLRGFLYYSLFEW  
FHPLFLEDESSSFHKRQFPVSKTLPELYELVNYYQPEVLWSDGDGGAPDQYWNSTGFLAWLY  
NESPVVRGTVVTNDRWGAGSICKHGGFYTCSDRYNPGHLLPHKWENCMTIDKLSWGYRREAGI  
SDYLTIEELVKQLVETVSCGGNLLMNIPTLDGTISVVFEERLRQVGWLKVNGEAIYETYT  
WRSQNNDTVTPDVWYTSPKPEKLVYAIFLKWPTSGQLFLGHPKAILGATEVKLLGHGQPLNWI  
SLEQNGIMVELPQLTIHQMPCKWGWLALTNVI

**Signal sequence:**

amino acids 1-28

**N-glycosylation site.**

amino acids 171-175, 239-243, 377-381

**Casein kinase II phosphorylation site.**

amino acids 32-36, 182-186, 209-213, 227-231, 276-280, 315-319,  
375-375

**Tyrosine kinase phosphorylation site.**

amino acids 361-369, 389-397

**N-myristoylation site.**

amino acids 143-149, 178-184, 255-261, 272-278, 428-434

**Leucine zipper pattern.**

amino acids 410-432

**Alpha-L-fucosidase putative active site.**

amino acids 283-295

## **FIGURE 73**

AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTAACATAGT  
TCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAAGTGGCCATC  
TGAGGTGTTCCCTGGCTCTGAAGGGTAGGCACGATGGGCAGGTGCTTCAGCCTGGTGTG  
CTTCTCACTTCCATCTGGACCACAGGGCTCTGGCCAAGGCTCTTGCAGCAGAAGAGCT  
TTCCATCCAGGTGTATGCAGAATTATGGGATCACCCCTGTGAGCAAAAGGCAGACCAGC  
AGCTGAATTACAGAAGCTAAGGAGGCCTGTAGGGCTGCTGGACTAAGTTGGCGGCAAG  
GACCAAGTTGAAACAGCCTGAAAGCTAGCTTGAAACTTGCAGCTATGGCTGGGTTGGAGA  
TGGATTCTGTGGTCATCTTAGGATTAGCCCCAACCCCAAGTGTGGAAAAATGGGTTGGGTG  
TCCTGATTGAAAGGTTCAGTGAGCCGACAGTTGCAGCCTATTGTTACAACATCTGAT  
ACTTGGACTAACTCGTGCATTCCAGAAATTATCACCACCAAAGATCCCATAATTCAACACTCA  
AACTGCAACACAAACACAAGAAATTATTGTCAAGTACAGTACACTCGGTGGCATCCCCTT  
ACTCTACAATACCTGCCCTACTACTACTCCTCTGCTCCAGCTTCAACTCTATTCCACGG  
AGAAAAAAATTGATTGTGTACAGAAGTTTATGAAACTAGCACCAGTCTACAGAAAC  
TGAACCATTGTTGAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTGGAGGTGTCC  
CCACGGCTCTGCTAGTGCTCTCCTCTTGGTGTGCAGCTGGTCTGGATTTC  
TATGTCAAAAGGTATGTGAAGGCCCTCCCTTTACAAACAAGAATCAGCAGAAGGAATGAT  
CGAAACCAAAAGTAGTAAAGGAGGAGAAGGCCAATGATAGCAACCTAATGAGGAATCAAAGA  
AAACTGATAAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAAACTACCGTGCATGCC  
GCTGAAGTTAGATGAGACAGAAATGAGGAGACACACCTGAGGCTGGTTCTTCATGCTCC  
TTACCCCTGCCCTAGCTGGGAAATCAAAGGGCAAAGAACCAAAGAACAGTCCACCC  
GGTTCTAACTGGAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCAAAGAGAAC  
CCTTCTCCTATTGTAACCCTGCTGGATCCTATCCTCCTACCTCCAAGCTTCCCACGGCC  
TTCTAGCCTGGCTATGTCTTAATAATATCCCACGGAGAACAGGAGTTGCAAAGTGCAA  
GGACCTAAACATCTCATCAGTATCCAGTGGTAAAAGGCCCTGGCTGTGAGGCTAGG  
TGGTTGAAAGCCAAGGAGTCAGGACTGAGACCAAGGCTTCTACTGATTCCGAGCTCAGAC  
CCTTCTCAGCTCTGAAAGAGAACACGTATCCCACCTGACATGCTCTGAGGCCGGTA  
AGAGAAAAGAACATGGCAGAAAAGTTAGCCCCTGAAAGCCATGGAGATTCTCATAAC  
ACCTAATCTCTGTAAGCTAAAGAACAGGCTGAGGATACGACAGTACACT  
GTCAGCAGGGACTGTAACACAGACAGGGCAAAGTGTCTCTGAACACATTGAGTTGGA  
ATCACTGTTAGAACACACACACTTACTTTCTGGTCTCTACCACTGCTGATATTCT  
AGGAAATATACTTTACAAGTAACAAAATAAAACTCTTATAAATTCTATTCT  
GTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTGTTAAAAGTAATAAAATTCA  
ACAAACATTGCTGAATAGCTACTATATGTCAGTGCTGTGCAAGGTATTACACTCTGTAAT  
TGAATTATTCTCTAAAAATTGCACTAGTAGAACGCTATCTGGGAAGCTATTCT  
GTTTGATATTCTAGCTTACTTCCAAACTAATTCTATTCT  
ATTCAATTCTCTAATATGGCAACCATTATAACCTTAATTATTAAACATACCTAAGAAC  
TACATTGTTACCTCTATATACCAAAGCACATTAAAAGGCCATTAACAAATGTATCACTA  
GCCCTCCTTTCCAACAAGAAGGGACTGAGAGATGCAGAAATATTGTGACAAAAATTAA  
AGCATTAGAAAACCTT

## **FIGURE 74**

MARCFSLVLLLTSIWTTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACR  
LLGLSLAGKDQVETALKASFETCSYGVGDGFVVISRISPNSPKCGKNGVGVLIWKPVSQF  
AAYCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPP  
APASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGGVPTALLVIALLFF  
GAAAGLGFCYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKTDKNPEESKSP  
SKTTVRCLAEAV

**Signal sequence:**

amino acids 1-16

**Transmembrane domain:**

amino acids 235-254

**N-glycosylation site.**

amino acids 53-57, 130-134, 289-293

**Casein kinase II phosphorylation site.**

amino acids 145-149, 214-218

**Tyrosine kinase phosphorylation site.**

amino acids 79-88

**N-myristoylation site.**

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

## **FIGURE 75**

AGATGGCGGTCTTGGCACCTCTAATTGCTCTCGTATTGGTGCACGACTTCACGATGG  
CTCGCCCAACCTTACTACCTCTGTCGGCCCTGCTCTGCTGCCCTACTCGTGAGGAA  
ACTGCCGCCGCTCTGCCACGGTCTGCCACCCAACCGGAAGACGGTAACCGTGTGACTTTG  
ACTGGAGAGAAGTGGAGATCCTGATGTTCTCAGTGCCATTGTGATGAGAAGAACCGCAGA  
TCCATCACTGTGGAGCAACATATAGGCAACATTTCATGTTAGTAAAGTGGCAACACAAT  
TCTTTCTTCCGCTGGATATTGCATGGCCTACTTACATCACACTCTGCATAGTGTCC  
TGATGACGTGCAAACCCCCCTATATATGGGCCCTGAGTATATCAAGTACTTCAATGATAAA  
ACCATTGATGAGGAACTAGAACGGGACAAGAGGGTCACTGGATTGTGGAGTTCTTGCAA  
TTGGTCTAATGACTGCCAATCATTGCCCTATCTATGCTGACCTCTCCCTAAATACAAC  
GTACAGGGCTAAATTTGGGAGGTGGATGTTGGACGCTACTGATGTTAGTACGGGTAC  
AAACTGAGCACATCACCCCTACCAAGCAACTCCCTACCCCTGATCCTGTTCCAAGGTGGCAA  
GGAGGCAATGCGGCGGCCACAGATTGACAAGAAAGGACGGCTGTCTCATGGACCTCTG  
AGGAGAATGTGATCCGAGAATTAACTTAAATGAGCTATACCAGCGGCCAAGAAACTATCA  
AAGGCTGGAGACAATATCCCTGAGGAGCAGCCTGTGGCTCAACCCCCACCACAGTGTCA  
TGGGAAAACAAGAAGGATAATAAGATCCTACTTGGCAGTGCTTCTCCTGTCAATT  
CCAGGCTTTCCATAACCACAAGCCTGAGGCTGCAGCCTTNATTNATGTTTCCCTTGG  
CTGNGACTGGNTGGGCAGCATGCAGCTCTGATTAAAGAGGCATCTAGGGATTGTCAG  
GCACCCCTACAGGAAGGCCTGCCATGCTGTGGCAACTGTTCACTGGAGCAAGAAAGAGATC  
TCATAGGACGGAGGGGAAATGGTTCCCTCCAAGCTGGTCAGTGTGTTACTGCTTATC  
AGCTATTGACACATCTCCATGGTTCTCCATGAAACTCTGTGGTTCATCATTCTCTTAG  
TTGACCTGCACAGCTGGTTAGACCTAGATTAAACCTAAGGTAAGATGCTGGGTATAGAA  
CGCTAAAGAATTTCACCCCAAGGACTCTGCTTCTTAAGCCCTCTGGCTTATGGTC  
TTCATTAAAAGTATAAGCCTAACTTGTGCTAGTCCTAAGGAGAACCTTAACCACAAAG  
TTTTATCATGAAGACAATATTGAACAAACCCCTATTTGTGGGATTGAGAAGGGGTGAA  
TAGAGGCTTGAGACTTCCCTTGTGTGGTAGGACTGGAGGAGAAATCCCCTGGACTTCAC  
TAACCCCTCTGACATACTCCCCACACCCAGTTGATGGCTTCCGTAATAAAAGATTGGGATT  
TCCTTTG

## **FIGURE 76**

MAVLAPLIALVYSVPRLSRWLAQPYYLLSALLSAAFLLVRKLPPLCHGLPTQREDGNPCDFD  
WREVEILMFLSAIVMMKNRRSITVEQHIGNIFMFSKVANTILFFRLDIRMGLLYITLCIVFL  
MTCKPPLYMGPEYIKYFNDKTIDEELERDKRVTWIVEFFANWSNDCQSFAPIYADLSLKYNC  
TGLNFGKVDVGRYTDVSTRYKVSTSPLTKQLPTLILFQGGKEAMRRPQIDKKGRAVSWTFSE  
ENVIREFNLNELYQRAKKLSKAGDNIPEEQPVASTPTVSDGENKKDK

**Signal sequence:**

amino acids 1-48

**Transmembrane domain:**

amino acids 111-125

**N-glycosylation site.**

amino acids 165-169, 185-189

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 154-158, 265-269

**Casein kinase II phosphorylation site.**

amino acids 51-55, 145-149, 245-249, 286-290, 288-292

**N-myristoylation site.**

amino acids 188-194, 225-231

**Myb DNA-binding domain repeat signature 1.**

amino acids 244-253

## FIGURE 77

GGACAGCTCGGGCCCCGAGAGCTCTAGCCGTGAGGAGCTGCCCTGGGACGTTGCCCTG  
GGGCCAGCCTGGCCGGTCACCCTGGCATGAGGAGATGGCCTGTCCTGGTCCA  
TTGCTCCTGCTGCCGGCTCCTACGGACTGCCCTCTACAACGGCTCTACTACTCCAACAG  
CGCCAACGACCAGAACCTAGGCAACGGTATGGCAAAGACCTCCTTAATGGAGTGAAGCTGG  
TGGTGGAGACACCGAGGAGACCCCTGTTCACCTACCAAGGGCCAGTGTGATCCTGCCCTGC  
CGCTACCGCTACGAGCCGGCCCTGGTCTCCC CGGGCGTGTGCGTCAAATGGTGAAGCT  
GTCGGAGAACGGGGCCCCAGAGAACGGACGTGCTGGTGCCATGGGCTGAGGCACCGCTCCT  
TTGGGACTACCAAGGCCCGTGCACCTGCGGCAGGACAAAGAGCATGACGTCTCGCTGGAG  
ATCCAGGATCTCGGCTGGAGGACTATGGCGTTACCGCTGTGAGGTATTGACGGCTGGA  
GGATGAAAGCGGTCTGGTGAGCTGGAGCTGCGGGGTGGTCTTCCCTAACAGTCCCCA  
ACGGCGCTACCAGTTCAACTTCCACGAGGGCCAGCAGGTCTGTGCAGAGCAGGCTGCCGTG  
GTGGCCTCCTTGAGCAGCTTCCGGCCTGGAGGAGGGCCTGGACTGGTGCAACGCCGG  
CTGGCTGCAGGATGCTACGGTGCAGTACCCCATCATGTTGCCCGGCAGCCCTGCCGTGGC  
CAGGCCTGGCACCTGGCGTGCAGCTACGGCCCCGCCACCGCCGCTGCACCGCTATGAT  
GTATTCTGCTCGCTACTGCCCTCAAGGGCGGGTGTACTACCTGGAGCACCCGTGAGAAGCT  
GACGCTGACAGAGGCAAGGGAGGCCTGCCAGGAAGATGATGCCACGATGCCAAGGTGGGAC  
AGCTCTTGCGCCTGGAAGTCCATGCCCTGGACCGCTGCGACGCTGGCTGGCTGGCAGAT  
GGCAGCGTCCGCTACCCGTGGTTACCCGCATCTAACTGTGGGCCCCAGAGCCTGGG  
CCGAAGCTTGGCTTCCCCGACCGCAGAGCCGCTGTACGGTGTACTGCTACCGCCAGC  
**A**C**T**AGGGACCTGGGCCCTCCCGCCATTCCCTACTGGCTGTGTATTGAGTGGTT  
CGTTTCCCTGTGGGTTGGAGCCATTAACTGTTTATACTTCTCAATTAAATTCT  
TTAACATTTTACTATTTTGAAAGCAAACAGAACCCATGCCCTCCCTGCTCCTG  
GATGCCCACTCCAGGAATCATGCTTGCCTCCCTGGGCCATTGCGGTTTGAGGCTCTG  
GAGGGTCCCCGCCATCCAGGCTGGCTCCCTCCCTTAAGGAGGTTGGTGCAGAGTGGC  
GGTGGCCTGTCTAGAATGCCGCCGGAGTCCGGCATGGTGGGCACAGTCTCCCTGCC  
CAGCCTGGGGAAGAAGAGGGCCTGGGGCCTCCGGAGCTGGCTTGGCCTCTGCC  
CACCTCTACTCTGTGAAGCCGCTGACCCAGTCTGCCACTGAGGGCTAGGGCTGGAA  
GCCAGTTCTAGGCTCAGGCAGAACATCTGAGGGAAGGAAGAAACTCCCTCCCCGTTCC  
TCCCTCTCGGTCCAAAGAACATCTGTTGTCATTGTTCTCCTGTTCCCTGTGTGG  
GGAGGGGCCCTCAGGTGTGTACTTGGACAATAATGGTGCTATGACTGCCCTCCGCAA  
AAA  
AAA

## **FIGURE 78**

MGLLLLVPLLLLPGSYGLPFYNGFYYSNSANDQNLGNHGKDLLNGVKLVVETPEETLFTYQ  
GASVILPCRYRYEPALVSPRRVRVKWWKLSENGAPEKDVLVAIGLRHRSFGDYQGRVHLRQD  
KEHDVSLEIQDLRLEDYGRYRCEVIDGLEDESGLVEELRGVVFPYQSPNGRYQFNFHEGQQ  
VCAEQAAVVASFEQLFRAWEELDWNCAGWLQDATVQYPIMLPRQPCGGPGLAPGVRSYGPR  
HRRLHRYDVFCFATALKGRVYYLEHPEKLTLTEAREACQEDDATIAKVGQLFAAWKFHGLDR  
CDAGWLADGSVRYPVVPVHPNCGPPEPGVRSFGFPDPQSRLYGVYCYRQH

**Signal sequence:**

amino acids 1-17

**Casein kinase II phosphorylation site.**

amino acids 29-33, 53-57, 111-115, 278-282

**Tyrosine kinase phosphorylation site.**

amino acids 137-145

**N-myristoylation site.**

amino acids 36-42, 184-190, 208-214, 237-243, 297-303, 307-313

## **FIGURE 79**

GGAGAGCGGAGCGAAGCTGGATAACAGGGGACCG**TGAT**GATGTGGCACCATCAGTTCTGCTGC  
TTCTGTTGCTACTGAGGCACGGGCCAGGGGAAGCCATCCCCAGACGCAGGCCCTCATGGC  
CAGGGGAGGGTGCACCAGGCAGCCCCCTGAGCGACGCTCCCCATGATGACGCCAACGGAA  
CTTCCAGTACGACCATGAGGCTTCCTGGACGGGAAGTGGCCAAGGAATTGACCAACTCA  
CCCCAGAGGAAAGCCAGGCCGTCTGGGCGGATCGTGGACCGCATGGACCGCGCGGGGAC  
GGCGACGGCTGGGTGTCGCTGCCGAGCTCGCGGTGGATCGGCACACGCAGCAGCGCA  
CATACGGGACTCGGTGAGCGCCGCTGGGACACGTACGACACGGACCGCGACGGCGTGTGG  
GTTGGGAGGAGCTGCGAACGCCACCTATGCCACTACGCACCGCTGGATCGAACAGGAA  
GTGGAGGATGCAGAGACCTACAAAAAGATGCTGGCTGGACGAGCGCGTTCGGGTGGC  
CGACCAGGATGGGACTCGATGCCACTCGAGAGGAGCTGACAGCCTCCTGCACCCCGAGG  
AGTTCCCTCACATGCCGACATCGTATTGCTGAAACCCCTGGAGGACCTGGACAGAAACAAA  
GATGGCTATGCCAGGTGGAGGAGTACATCGCGATCTGTACTCAGCCGAGCCTGGGAGGA  
GGAGCCGGCGTGGGTGCAGACGGAGAGGCAGCAGTCCGGACTTCCGGATCTGAACAAGG  
ATGGGCACCTGGATGGGAGTGAGGTGGCCACTGGGTGCTGCCCTGCCAGGACCAGCCC  
CTGGTGGAAGCCAACCAACCTGCTGCACGAGAGCGACACGGACAAGGATGGCGCTGAGCAA  
AGCGGAAATCCTGGTAATTGGAACATGTTGTGGCAGTCAGGCCACCAACTATGGCGAGG  
ACCTGACCCGGCACCAACGATGAGCTG**TGAG**CACCGCGCACCTGCCACAGCCTCAGAGGCCCG  
CACAAATGACCGGAGGAGGGGCCGTGGTCTGGCTGCCCTCCCTGTCCAGGCCCGCAGGAG  
GCAGATGCAGTCCCAGGCATCCTCCTGCCCTGGCTCTCAGGGACCCCTGGTCGGCTTC  
TGTCCCTGTACACCCCCAACCCAGGGAGGGCTGTCATAGTCCCAGAGGATAAGCAATAC  
CTATTCTGACTGAGTCTCCCAGCCCAGACCCAGGGACCCCTGGCCCAAGCTCAGCTCTAA  
GAACCGCCCCAACCCCTCCAGCTCCAAATCTGAGCCTCCACACATAGACTGAAACTCCCCT  
GGCCCCAGCCCTCTCCTGCCTGGCCTGGACACCTCCTCTGCCAGGAGGAATAA  
AAGCCAGCGCCGGGACCTTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAA

## **FIGURE 80**

MMWRPSVLLLLLRLHGAQGKPSDAGPHQGRVHQAPLSDAPHDDAHGNFQYDHEAFLGR  
EVAKEFDQLTPEESQARLGRIVDRMDRAGDGWVSLAELRAWIAHTQQRHIRDSVSAAWDT  
YDTDGRVGWEELRNATYGHYAPGEFHDVEDAETYKKMLARDERRFRVADQDGDSMATRE  
ELTAFLHPEEFPHMRDIVIAETLEDLDRNKGYVQVEEYIADLYSAEPGEEPAWVQTERQQ  
FRDFRDLNKGHDGSEVGHVLPPAQDQPLVEANHLLHESDTDKDGRLSKAEILGNWNMFV  
GSQATNYGEDLTRHHDEL

**Signal sequence:**

amino acids 1-20

**N-glycosylation site.**

amino acids 140-144

**Casein kinase II phosphorylation site.**

amino acids 72-76, 98-102, 127-131, 184-188, 208-212, 289-293,  
291-295, 298-302

**N-myristoylation site.**

amino acids 263-269, 311-317

**Endoplasmic reticulum targeting sequence.**

amino acids 325-330

## **FIGURE 81**

GGGGCCTTGCCTCCGCACTCGGGCGCAGCCGGTGGATCTCGAGCAGGTGCGGAGCCCCGG  
GCGGGGGCGCGGGTGCAGGGATCCCTGACGCCTCTGCCCTGTTCTTGTCGCTCCCAG  
CCTGTCGTCGTTGGCCCCCGCTCCCGCGGTGCGGGGTTGCACACCGATCCTG  
GGCTCGCTCGATTTGCCGCCAGGCGCTCCAGACCTAGAGGGCGCTGCCCTGGAGCAG  
CGGGTCGTCGTTGCCCTCTGCCGCCGGGATCCGAAGGGTGCGGGGCTCT  
GAGGAGGTGACGCCGGGCCTCCGCACCCTGCCATTCTCCCTCTCCCAG  
GTGTGAGCAGCCTATCAGTACCAATGTCCGCAGCCTGGATCCCGCTCTGCCCTGGTGTG  
TGTCTGCTGCTGCCGGGCCGCGGGCAGCGAGGGAGCCGCTCCATTGCTATCACATG  
TTTACCAAGGGCTTGGACATCAGGAAAGAGAAAGCAGATGTCCTCTGCCAGGGGCTGCC  
CTCTGAGGAATTCTCTGTATGGGAACATAGTATATGCTCTGTATCAGCATATGTGGG  
GCTGCTGTCACAGGGAGTAATCAGCAAATCAGGGGACCTGTACGAGTCTATAGCCTACC  
TGGTCGAGAAAATATTCTCAGTAGATGCCAATGGCATCCAGTCTCAAATGCTTCTAGAT  
GGTCTGCTTCTTCACAGTAACTAAAGCAGGAAAGTAGTACACAGGAGGCCACAGGACAAGCA  
GTGTCCACAGCACATCCACCAACAGGTAACAGACTAAAGAAAACACCCGAGAAGAAAATGG  
CAATAAGATTGAAAGCAGACATTGCATTCTGATTGATGGAAGCTTAATATTGGCAGC  
GCCGATTTAATTACAGAAGAATTGTTGGAAAAGTGGCTCTAATGTTGGAAATTGAAACA  
GAAGGACCACATGTGGCCTTCAAGCCAGTGAACATCCAAATAGAATTACTGAA  
AAACTTACATCAGCCAAAGATGTTGTCATAAAGGAAGTAGGTTCAGAGGGGTA  
ATTCCAATACAGGAAAAGCCTTGAAGCATACTGCTCAGAAATTCTCACGGTAGATGCTGGA  
GTAAGAAAAGGGATCCCAAAGTGGTGGTATTATTGATGGTGGCTCTGATGACAT  
CGAGGAAGCAGGCATTGTGGCCAGAGAGTTGGTGTCAATGTATTATAGTTCTGTTG  
AGCCTATCCCTGAAGAACCTGGGATGGTCAGGATGTCACATTGTTGACAAGGCTGCTGT  
CGGAATAATGGCTTCTTCTTACACATGCCAACTGGTTGGCACCACAAAATACGTAA  
GCCTCTGGTACAGAACAGCTGTGCACTCATGAACAAATGATGTGCAGCAAGACCTGTTATAACT  
CAGTGAACATTGCTTCTAATTGATGGCTCCAGCAGTGTGGAGATAGCAATTCCGCTC  
ATGCTGAATTGTTCCAACATAGCCAAGACTTTGAAATCTGGACATTGGTGCAGAT  
AGCTGCTGTACAGTTACTTATGATCAGCGCACGGAGTTCAGTTCACTGACTATAGCACCA  
AAGAGAATGTCTTAGCTGTCACTAGAAACATCCGCTATATGAGTGGTGGAACAGCTACTGGT  
GATGCCATTCTTCACTGTTAGAAATGTGTTGGCCCTATAAGGGAGAGCCCCAACAGAA  
CTTCCTAGTAATTGTCACAGATGGCAGTCCTATGATGATGTCCAAGGCCCTGCAGCTGCTG  
CACATGATGCAGGAATCACTATCTCTGTTGGTGTGGCTGGCACCTGGATGACCTG  
AAAGATATGGCTCTAAACCGAAGGAGTCTCACGCTTCTCACAGAGAGTTCACAGGATT  
AGAACCAATTGTTCTGATGTCACTAGAGGCATTGTTAGAGATTCTTAGAATCCCAGCAAAT  
AATGGAACATTGACAACAGAAAGAAAAGTACAAGGGATCCAGTGTGAAATTGTATT  
CTCATAATACTGAAATGCTTCACTAGCATACTAGAATCAGATACAAACTATTAAGTATGTCAAC  
AGCCATTAGGCAAATAAGCACTCCTTAAAGCCGCTGCCCTGTTACAATTACAGTGT  
ACTTGTAAAAACACTGCTGAGGCTTCATAATCATGGCTTCAAGAAACTCAGGAAAGAGGA  
GATAATGTGGATTAAAACCTTAAGAGTTCAACCAGCCTACTAAATGTACAGATATGCAA  
TTCCATAGCTCAATAAGAACATCTGATACTTAGACCAAAAAAA

## **FIGURE 82**

MSAAWIPALGLGVCLLLPGPAGSEAAPIAITCFTRGLDIRKEKADVLCPGGCPLLEFSVY  
GNIVYASVSSICGAAVHRGVISNSGGPVRYSLPGRENYSSVDANGIQSQMLSRWSASFTVT  
KGKSSTQEATGQAVSTAHPPTGKRLKKTPEKKTGNKDCKADIAFLIDGSFNIQQRNFNLQKN  
FVGKVALMLGIGTEGPHVGLVQASEHPKIEFYLNFTSAKDVLFAIKEVGFRGGNSNTGKAL  
KHTAQKFFTVDAGVRKGIPKVVVFIDGWPSDDIEEAGIVAREFGVNVFIVSVAKPIPEELG  
MVQDVTFVDKAVCRNNNGFFSYHMPNWFGTTKYVKPLVQKLCTHEQMMCSKTCYNSVNIAFLI  
DGSSSGDSNFRLMLEFVSNIAKTFEISDIGAKIAAVQFTYDQRTEFSFTDYSTKENVLAVI  
RNIRYMSGGTATGDAISFTVRNVFGPIRESPNKNFLVIVTDGQSYDDVQGPAAAHDAGITI  
FSVGVAWAPLDDLKDMASKPKESHAFFTREFTGLEPIVSDVIRGICRDFLESQQ

**Signal sequence:**

amino acids 1-24

**N-glycosylation site.**

amino acids 100-104, 221-225

**Casein kinase II phosphorylation site.**

amino acids 102-106, 129-133, 224-228, 316-320, 377-381, 420-424,  
425-429, 478-482, 528-532

**N-myristoylation site.**

amino acids 10-16, 23-29, 81-87, 135-141, 158-164, 205-211,  
239-245, 240-246, 261-267, 403-409, 442-448, 443-449

**Amidation site.**

amino acids 145-149

## **FIGURE 83**

CGCCGCCTCCGCACCGCGGCCACCGCGCCGCTCCGCATCTGCACCCGAGCCC  
GGCggcctccggggagcgagcagatccagtcggccgcagcgcaactcggtccagtcg  
GGGCGGGCTGCGGGCGCAGAGCGGATGCAGCGGCTGGGCCACCTGCTGCCTGC  
TGCTGGCGGGCGGTCCCCACGGCCCCCGCGCTCGACGGCGACCTCGGCTCAGTC  
AAGCCGGCCGGCTCTCAGTACCCGAGGAGGCCACCTCAATGAGATGTTCCGCGA  
GGTTGAGGAACTGATGGAGGACACGCAGCACAAATTGCGCAGCGGGTGGAAAGAGATGGAGG  
CAGAAGAAGCTGCTGCTAAAGCATCATCAGAAGTGAACCTGGCAAACCTACCTCCCAGCTAT  
ACAATGAGACCAACACAGACAGAAGGTTGAAATAATACCACATGTGCACCGAGAAAT  
TCACAAGATAACCAACAACCAGACTGGACAAATGGTCTTTCAGAGACAGTTATCACATCTG  
TGGGAGACGAAGAAGGAGAAGGAGCCACGAGTCATCATCGACGAGGACTGTGGGCCAGC  
ATGTACTGCCAGTTGCCAGCTTCCAGTACACCTGCCAGCCATGCCGGGCCAGAGGATGCT  
CTGCACCCGGGACAGTGAGTGCTGTGGAGACCAGCTGTGTCTGGGGTCACTGCACCAAAA  
TGGCCACCAGGGGAGCAATGGGACCATCTGTGACAACCAGAGGGACTGCCAGCCGGGCTG  
TGCTGTGCCTTCCAGAGAGGCCCTGCTGTTCCCTGTGTGCACACCCCTGCCCGTGGAGGGAG  
GCTTGCCATGACCCGCCAGCCGGCTCTGGACCTCATCACCTGGAGCTAGAGCCTGATG  
GAGCCTGGACCGATGCCCTGTGCCAGTGGCCTCCTCTGCCAGCCCCACAGCCACAGCCTG  
GTGTATGTGCAAGCCGACCTCGTGGGGAGCCGTGACCAAGATGGGAGATCCTGCTGCC  
CAGAGAGGTCCCCGATGAGTATGAAGTGGCAGCTTATGGAGGAGGTGCCAGGAGCTGG  
AGGACCTGGAGAGGGAGCCTGACTGAAGAGATGGCGCTGGGGAGCCTGCCGCTGCCGCGCT  
GCACTGCTGGGAGGGAGAGATTTAGATCTGGACCAAGGCTGTGGTAGATGTGCAATAGAA  
ATAGCTAATTATTCCCCAGGTGTGCTTAGGCGTGGCTGACCAGGCTTCTTCTACA  
TCTTCTTCCCAGTAAGTTCCCTCTGGCTTGACAGCATGAGGTGTTGTGCATTGTCAGC  
TCCCCCAGGCTGTTCTCCAGGCTTCACAGTCTGGCTGGAGAGTCAGGCAGGGTTAAC  
TGCAGGAGCAGTTGCCACCCCTGTCCAGATTATTGGCTGCTTGCCTCTACCAGTGGCAG  
ACAGCCGTTGTTCTACATGGCTTGATAATTGTTGAGGGAGGAGATGAAACAATGTGG  
AGTCTCCCTCTGATTGGTTGGGAAATGTGGAGAAGAGTGCCTGCTTGCAAACATCAA  
CCTGGAAAAATGCAACAAATGAATTTCACGCAGTTCTTCCATGGCATAGGTAAGCTG  
TGCCTTCAGCTGTTGCAAGATGAAATGTTCTGTTACCCCTGCATTACATGTGTTATTCTAC  
AGCAGTGTGCTCAGCTCCTACCTCTGTGCCAGGGCAGCATTTCATATCCAAGATCAATT  
CCTCTCTCAGCACAGCCTGGGGAGGGGTCAATTGTTCTCCTCGTCATCAGGGATCTCAGAG  
GCTCAGAGACTGCAAGCTGCTGCCAAGTCACACAGCTAGTGAAGACCAGAGCAGTTCAT  
CTGGTTGTGACTCTAACGCTCAGTGCTCTCCACTACCCACACCAGCCTGGTGCCACCAA  
AAGTGTCCCCAAAAGGAAGGAGAATGGGATTTCCTGAGGCATGCACATCTGGAATTAAG  
GTCAAACTAATTCTCACATCCCTCTAAAGTAAACTACTGTTAGGAACAGCAGTGTCTCAC  
AGTGTGGGGCAGCGTCTTCTAATGAAGACAATGATATTGACACTGTCCCTTTGGCAGT  
TGCATTAGTAACTTGAAGGTATGACTGAGCGTAGCATACAGGTTAACCTGCAGAAACA  
GTACTTAGGTAATTGTAGGGCGAGGATTATAAATGAAATTGCAAATCAGTACAGCAAC  
TGAAGACAATTATCAACCACGTGGAGAAAATCAAACCGAGCAGGGCTGTGAAACATGGTT  
GTAATATGCGACTGCAACACTGAACTCTACGCCACTCCACAAATGATGTTTCAGGTGTCA  
TGGACTGTTGCCACCATGTATTCAAGAGTTCTAAAGTTAAAGTTGCAACATGATTGTA  
TAAGCATGCTTCTTGAGTTAAATTATGTATAAACATAAGTGCATTAGAAATCAAGC  
ATAAAACTTCAACTGCAAAAAAAAAAAAAAA

## **FIGURE 84**

MQRLGATLLCLLLAAAVPTAPAPAPTATSAPVKPGPALSYPQEEATLNEMFREVEELMEDTQ  
HKLRSAVEEMEAEAAAAKASSEVNLANLPPSYHNETNTDKVGNNTIHVHREIHKITNNQTG  
QMVFSETVITSVGDEEGRRSHECIIDEDCGPSMYCQFASFQYTCQPCRQMLCTRSECCG  
DQLCVWGHCTKMATRGSGNTICDNQRDCQPGLCCAFQRGLFPVCTPLPVEGELCHDPASRL  
LDLITWELEPDGALDRPCASGLLCQPHSHSLVYVCKPTFVGSRDQDGEILLPREVPDEYEV  
GSFMEEVVRQELEDLERSLTEEMALGEPAAAAALLGGEI

**Signal sequence:**

amino acids 1-19

**N-glycosylation site.**

amino acids 96-100, 106-110, 121-125, 204-208

**Casein kinase II phosphorylation site.**

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,  
327-331

**N-myristoylation site.**

amino acids 202-208, 217-223

**Amidation site.**

amino acids 140-144

## **FIGURE 85**

AAGGAGGCTGGGAGGAAAGAGGTAAAGAAAGGTTAGAGAACCTACCTCACATCTCTGGGCTCAGAAGGACTCTG  
AAGATAACAATAATTTCAGCCCATCCACTCTCCTTCCCAAACACACATGTGCATGTACACACACACATACA  
CACACATACACCTTCCCTCTTCACTGAAGACTCACAGTCACTCACTCTGTGAGCAGGTATAGAAAAGGACAC  
TAAAGCCTTAAGGACAGGCTGGCATTACCTCTGCAGCTCTTGGTTGAGTCAAAAAACATGGGAGGG  
CCAGGCACGGTACTCACACCTGAATCCCAGCATTTGGAGACCGAGGTGAGCAGATCACTTGAGGTCAAGGAG  
TTCGAGACCAGCCTGCCAACATGGAGAAACCCCCATCTCTACTAAAAATACAAAAATTAGCCAGGAGTGGTGGC  
AGGTGCCTGTAATCCCAGCTACTCAGGTGGCTGAGCCAGGAGAACGTTGAATCCAGGAGGCGAGGATGCAGT  
CAGCTGAGTGCACCGCTGCACTCCAGCCTGGGTGACAGAACGAGACTCTGTCTCAAACAAACAAACACGGAGGA  
GGGGTAGATACTGCTTCTCTGCAACCTCTTAACTCTGCATCCTCTTCCAGGGCTGCCCTGATGGGCGCTG  
GCAATGACTGAGCAGGCCAGCCCCAGAGGAACAAGGAAGAGAACGGATATTGAGGAGGGCAAGAAGTGA  
GCCCCCGGTGAGGAGGGTGGTCTGGGCCCTGGCAGGGTTGCTGACCCCTACCCCTGCAAAACACA  
AAGAGCAGGACTCCAGACTCTCTTGTGAATGGTCCCCTGCCCTGAGCCTCCACATGAGGCTTCTCGTGG  
ACTCTGCTAGCTTGGGTGGCTGGTGCCTGCACTGTGCCACTGTGCCGTGGTACCTGCACTGTTCC  
GTGTGCCTGCCAGATCCGGCCCTGGTATACGCCCGCTGCTTACCGCAGGCTACCAACTGTGGACTGCAATGA  
CCTATTCTGACGGCAGTCCCCCGGCACTCCCCGAGGCACACAGACCCCTGCTCTGCAGAGCAACAGCATTGT  
CCGTGTGGACCAGAGTGAGCTGGTCACTGGCCAATCTCACAGAGCTGGACCTGTC  
CAGCCTGAGGAGACTGTGATTCCATGCCCTGCCAGCTGCTGAGCCTGACCTAGAGGAGAAC  
GGAGGACCACAGCTTGCAAGGCTGGCAGCCTACAGGAACCTATCTCAACCACACCAGCTTACCGCATCGC  
CCCCAGGGCTTTCTGGCTCAGCAACTTGCTGGCTGACCTCAACTCCAACCTCTGAGGGCATTGACAG  
CCGCTGGTTGAAATGCTGCCAACTGGAGATACTCATGATTGGCGCAACAAGGTAGATGCCATCTGGACAT  
GAACCTCCGGCCCTGGCAACCTGCGTAGCCTGGTCTAGCAGGCACTGAACCTGCCGGAGATCTCGACTATGC  
CCTGGAGGGCTGCAAAGCTGGAGAGCCTCTCTATGACAACACCAGCTGGCCGGGTGCCAGGCGGGCACT  
GGAACAGGTGCCGGGCTCAAGTCCCTAGACCTCAACAAGAACCCGCTCCAGCAGGGTAGGGCCGGGGACTTGC  
CAACATGCTGCACCTTAAGGAGCTGGACTGAACAAACATGGAGGAGCTGGTCTCATCGACAAGTTGCC  
GAACCTCCCCGAGCTGACCAAGCTGGACATCACCAATAACCCACGGCTGCTTACCCACCCCCGGCCTTCCA  
CCACCTGCCCAAGATGGAGAACCTCATGCTCAACAAACACGCTCTCAGTGCCTGCCACAGCAGGGTGGAGTC  
CCTGCCCAACCTGCAGGAGGTAGGTCTCCACGGCAACCCCATCGCTGTGACTGTGTCATCCGCTGGGCAATGC  
CACGGGACCCGTGTCCGCTTACCGAGCCCAATCCACCCCTGTGTGCGGAGCCTCCGGACCTCCAGCGCTCCC  
GGTCCTGAGGTGCCCTTCGGAGATGACGGACCACTGTTGCCCTCATCTCCCCACGAAGCTCCCCAAG  
CCTCCAGGTAGCCAGTGGAGAGAGCATGGTGTGCAATTGCCGGCACTGGCGAACCCGAACCGAGATCTACTG  
GGTCACTCCAGCTGGGCTTCGACTGACACCTGCCATGCAGGCAAGGAGTACCGGGTGTACCCGAGGGGACCC  
GGAGCTGGAGGGTACAGCAGAACAGGGCAGGGCTATACACCTGTGTGCCCAGAACCTGGTGGGGCTGACAC  
TAAGACGGTTAGTGTGGTTGTGGCCGTCTCCTCCAGCCAGGCAAGGACAGGGGCTGGAGCTCCG  
GGTGCAGGAGACCACCCCTATCACATCCTGCTATCTGGTCACCCACCCAAACACAGTGTCCACCAACCTCAC  
CTGGTCCAGTGCCTCCCTCCGGGCCAGGGGCCACAGCTCTGGCCGCTGCCTGGGAACCCACAGCTA  
CAACATTACCGCCTCCCTCAGGCCACGGAGTACTGGCCTGCCATGCAAGTGGCTTGTGATGCCACACCCA  
GTTGGCTGTATGGGCCAGGACCAAAGAGGCCACTCTTGCACAGAGCCTTAGGGATGTCCTGGCTCAT  
TGCCATCCTGGCTCTCGCTGTCCCTCTCTGGCACTGGCTAGCGGCCACCTTGGCACAGGCAACCCAGGAA  
GGGTGGTGGGAGGGCCCTCTCCAGCTGGCTTCTGGGCTGGAGTGCCTTCTGTCCGGTTGT  
GTCTGCTCCCTCGTCCTGCCCTGGAAATCCAGGGAGGAACCTGCCCAGATCTCAGAAGGGAGACACTGTTGCC  
ACCATTGTCTCAAATTCT**TGAAGCTCAGCCTGTTCTCAGCAGTAGAGAACATCACTAGGACTACTTTTAC**  
AAA  
AGAGAACAGTCTGGGCCAGATGCCCTGCCAGGAAAGGGACATGGACCCACGTGCTTGAGGGCTGGCAGCTGGC  
CAAGACAGATGGGCTTTGTGGCCCTGGGGGTGCTCTGGCAGGCTTGAAGGAAGTTGCCCTTACCTCCTAGGGTCA  
CCTCTGCTGCCATTCTGAGGAACATCTCAAGGAACAGGGAGACTTGGCTAGAGCCTCTGCCTCCCATCT  
CTCTCTGCCAGGGCTCTGGCCTGGCTTGGCTTACCTGTGTCCTCCGGCTGCAACCCCTTCTCTTC  
TCTTCTCTGTACAGTCTCAGTTGCTTGTGCTCTGGCAAGGGCTGAAGGAGGCCACTCCATCTCAC  
CTCGGGGGCTGCCCTCAATGTGGAGGTGACCCAGCCAGATCTGAAGGAACATTGGAGAGGGATGCCAGGAA  
CGCCTCATCTCAGCAGCCTGGCTGGCATTCCGAAGCTGACTTTCTATAGGCAATTGTACCTTGTGGAGAA  
ATGTGTACACCTCCCCAACCCGATTCACTCTTCTCTGTAAAAATAAAATAACAATAAAA  
AAAA

## **FIGURE 86**

MRLLVAPLLLAWVAGATAATPVVPWHVPCPPQCACQIRPWYTPRSSYREATTVDNDLFLTA  
VPPALPAGTQTLLLQSNSIVRVDQSELGYLANLTELDLSQNSFSDARCDFHALPQLLSLHL  
EENQLTRLEDHSFAGLASLQELYLNHNQLYRIAPRAFSGLSNLLRLHLSNLLRAIDSRWFE  
MLPNLEILMIGGNKVDAILDMDNFRPLANLRSVLVLAGMNLREISDYALEGLQSLSFYDNQ  
LARVPRRALEQVPGLKFLDLNKNPLQRVGPGDFANMLHLKELGLNNMEELVSIDKFALVNLP  
ELTKLDITNNPRLSFIHPRAFHLPQMETLMLNNNALSHQQTVESLPNLQEVGLHGNPIR  
CDCVIRWANATGTRVRFIEPQSTLCAEPPDLQRLPVREVPFREMTDHCLPLISPRSFPPSLQ  
VASGESMVLHCRALAEPEIYWVTPAGLRLTPAHAGRRYRVYPEGTLELRRVTAAEAGLYT  
CVAQNLVGADTKTVVVGRALLQPGRDEQGLELRVQETHPYHILLSWTPNNTVSTNLTW  
SSASSLRGQQGATALARLPRGTHSYNITRLLQATEYWACLOVAFADAHTQLACWARTKEATS  
CHRALGDRPGLIAILALAVLLAAGLAHLGTQPRKGVGGRPLPPAWAFWGWSAPSVRVV  
SAPIVLPWNPGRKLPRSSEGETLLPPLSQNS

**Signal sequence:**

amino acids 1-18

**Transmembrane domain:**

amino acids 629-648

**N-glycosylation site.**

amino acids 94-98, 381-385, 555-559, 583-587

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 485-489

**Casein kinase II phosphorylation site.**

amino acids 46-50, 51-55, 96-100, 104-108, 130-134, 142-146,  
243-247, 313-317, 488-492, 700-704

**Tyrosine kinase phosphorylation site.**

amino acids 532-540

**N-myristoylation site.**

amino acids 15-21, 493-499, 566-572

**Amidation site.**

amino acids 470-474, 660-664, 692-696

## **FIGURE 87**

GCAAGCCAAGGCCGCTGTTGAGAAGGTGAAGAAGTCCGGACCCATGTGGAGGAGGGGACATTGTGTACCGCCT  
CTACATGCGGCAGACCATCATCAAGGTGATCAAGTTCATCTCATCATCTGCTACACCGTCTACTACGTGCACAA  
CATCAAGTTCGACCGTGGACTGCACCGTGGACATGTGAGAGCCTGACGGGCTACCGCACCTACCGCTGTGCCACCC  
CCTGGGCCACACTCTTCAGATCCTGGCGCTCTTCTACATCAGCCTAGTCATCTTACGGCCTCATCTGCATGTA  
CACACTGTGGTGGATGCTACGGCGCTCCCTCAAGAAGTACTCGTTGAGTCGATCCGTGAGGAGAGCAGCTACAG  
CGACATCCCCGACGTCAAGAACGACTTCGCTTCTCATGCTGCACCTCATGACCAATAACGACCCGCTCTACTCCAA  
GCGCTTCGCCGCTTCTCTGCGAGGTGAGTGAGAACAGCTGCGGCAGCTGAACCTCAACAACAGTAGTGGACGCT  
GGACAAGCTCCGGCAGCGGCTCACCAAGAACGCGCAGGACAAGCTGGAGCTGCACCTGTCATGCTCAGTGGCAT  
CCCTGACACTGTGTTGACTGGTGGAGCTGGAGGTCTCAAGCTGGAGCTGATCCCCGACGTGACCATCCCCGCC  
CAGCATTGCCAGCTCACGGGCCTCAAGGAGCTGAGCTTACACACAGCGGCCAAGATGAGTCAGCGCCTGCGCT  
GGCCTTCCTGCGCGAGAACCTGCGGGCGCTGCACATCAAGTTACCGACATCAAGGAGATCCCCTGTTGAGCTA  
TAGCCTGAAGACACTGGAGGAGCTGACCTGACGGGCAACTGAGCGGGAGAACACCGCTACATCGTCACTGA  
CGGGCTGCGGGAGCTCAAACGCCCTCAAGGTGCTGCGGCTCAAGAGCAACCTAACGAAAGCTGCCACAGGTGGTCAC  
AGATGTGGCGTGCACCTGCGAGACTGTCCATCAACAAATGAGGGCAGCAAGCTCATCGTCTTCAACAGCCTCAA  
GAAGATGGCGAACCTGACTGAGCTGGAGCTGATCCGCTGCGACCTGGAGCGCATCCCCACTCCATCTTCAGCCT  
CCACAAACCTGCAAGGAGATTGACCTCAAGGACAACACCTCAAGACCATCGAGGAGATCATCAGCTTCCAGCACCT  
GCACCGCCTCACCTGCCCTAACGCTTAAAGCTGTTACAACCACATGCCCTACATCCCCATCCAGATCGGCAACCTCACCA  
CCTGGAGCGCCTTACCTGAACCGCAACAAGATCGAGAAGATCCCCACCCAGCTCTTCTACTGCCGCAAGCTGCG  
CTACCTGGACCTCAGCCACAAACCTGACCTTCTCCCTGCCGACATCGGCCCTCTGCGAGAACCTCCAGAACCT  
AGCCATCACGGCAACCGGATCGAGACGCTCCCTCCGGAGCTTCCAGTGCAGGAGCTGACGAGATCGAGCTGCGGGG  
GGGCAACAACGTGCTGCAGTCAGTGCCTCCAGGGTGGCGAGCTGACCAACCTGACGAGATCGAGCTGCGGG  
CAACCGGCTGGAGTGCCTGCCGTGGAGCTGGCGAGTGCCCAGTGCTCAAGCGCAGCGGCTGGTGGAGGA  
GGACCTGTTCAACACACTGCCACCCGAGGTGAAGGAGCGGCTGTGGAGGGCTGACAAGGAGCAGGCTGAGCGAG  
GCCGGGCCAGCACAGCAAGCAGCAGGACCGCTGCCAGTCTCAGGCCCCGAGGGCAGGCCAGTCTCTCCAG  
AACTCCGGACAGCCAGGACAGCCTCGGGCTGGCAGGGAGCCTGGGGCGTTGTGAGTCAGGCCAGAGCGAGA  
GGACAGTATCTGTTGGGCTGGCCCTTTCTCCCTCTGAGACTCACGTCCCCCAGGGCAAGTGTGGAGGAG  
AGCAAGTCTCAAGAGCGCAGTATTGATAATCAGGGCTCCTCCCTGGAGGCCAGCTCTGCCCTGGGCTGAG  
CTGCCACCAGAGGCTCTGGGACCCCTACTTTAGTTCTGGTATTATTCTCCATCTCCACCTCCTCATCC  
AGATAACTTATACATTCCCAAGAAAGTTCAGGCCAGATGGAAGGTGTTCAAGGAAAGGTGGCTGCCCTTTCCCC  
TTGTCTTATTAGCGATGCCGCCGGCATTTAACACCCACCTGGACTTCAGCAGAGTGGTCCGGGGCAACCCAG  
CCATGGGACGGTCACCCAGCAGTGCGGGCTGGCTCTGCGGTGCCACGGAGAGCAGGCCCTCCAGCTGGA  
AAGGCAGGCCCTGGAGCTTGCTCTCAGTTTGTGGCAGTTAGTTTTGTGTTTTTTTAATCAAA  
AAACAATTTTTAAAGCTTGAAGGGATGGTTGGGTTATTAAAAGAAAAAAACTTAAAAAAA  
AAAAGACACTAACGGCCAGTGAGTTGGAGTCTCAGGGCAGGGTGGCAGTTCCCTTGAGCAAGCAGCCAGACGT  
TGAACGTGTTCTTCCCTGGGCCAGGGTGCAGGGTGTCTTCCGGATCTGGTGTGACCTGGTCCAGGAGTT  
CTATTGTTCTGGGAGGGAGGTTTTGTGTTGGGTTTTGGTGTCTTGTGTTCTTCTCC  
ATGTGTCTTGGCAGGCACTATTCTGTGGCTGTCGGCCAGAGGAATGTTCTGGAGCTGCCAAGGAGGGAGGAG  
ACTCGGGTTGGCTAATCCCCGATGAACGGTGCCTCATTGCCACCTCCCTCTGCGCTGCCCTGCCCTCTCCA  
CGCACAGTGTAAAGGAGCCAAGAGGAGCCACTTCGCCAGACTTGTGTTCCCCACCTCCCTGGGCATGGGTGTG  
CCAGTGCCACCGCTGGCTCCGCTGCTTCCATCAGCCCTGTCGCCACCTGGCTTCAAGAGCAGACACTTA  
GAGGCTGGTGGGAATGGGAGGTGCGCCCTGGAGGGCAGGCAGGGTGGTCCAAGCCGGTTCCCTGGCG  
CTGGAGTGACACAGCCCAGTCGGCACCTGGTGGCTGGAGGCCAACCTGCTTGTGTTAGATCACTCGGGTCCCCACCTT  
AGAAGGGTCCCCGCCCTAGATCAATCACGTGGACACTAAGGCACGTTTAGAGTCCTTGTCTTAATGATTATGT  
CCATCCGTCTGTCGGTCCATTGTGTTCTGCGTGTCAATTGGATATAATCCTCAGAAATAATGCACACTAG  
CCTCTGACAACCATGAAGCAAAAATCGTTACATGTGGGTCTGAACCTGTAGACTCGGTACAGTATCAAATAAA  
ATCTATAACAGAAAAAAAAAAAAAA

## **FIGURE 88**

MRQTIIKVIKFILIIICYTVYYVHNIKFVDVDCTVDIESLTGYRTYRCAHPLATLFKILASFYI  
SLVIFYGLICMYTLWWMLRRSLKKYSFESIREESSYSDIPDVKNDFAFMLHLIDQYDPLYSK  
RFAVFLSEVSENKLRLQLNLNNEWTLDKLQRQLTKNAQDKLELHLFMLSGLPDTVFDLVELEV  
LKLELIPDVTIPPSIAQLTGLKELWLYHTAAKIEAPALAFLRENLRALHIKFTDIKEIPLWI  
YSLKTLEELHLTGNLSAENNRYIVIDGLRELKRLKVLRLKSNLSKLPQVVTDVGVHLQKLSI  
NNEGTKLIVLNSLKKMANLTELELIRCDLERIPHISIFSLHNLQEIDLKDNNLKTIEEIISFQ  
HLHRLTCLKLWYNHIAYIPIQIGNLTNERLYLNRNKIEKIPTQLFYCRKLRYLDLSHNNLT  
FLPADIGLLQNLQNLAITANRIETLPPELFQCRKLRALHGNNVLQSLPSRVGELTNLTOIE  
LRGNRLECLPVELGECPPLLKRSGLVVEEDLFNTLPPEVKERLWRADKEQA

**Transmembrane domain:**

amino acids 51-75 (type II)

**N-glycosylation site.**

amino acids 262-266, 290-294, 328-332, 396-400, 432-436, 491-495

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 85-89

**Casein kinase II phosphorylation site.**

amino acids 91-95, 97-101, 177-181, 253-257, 330-334, 364-368,  
398-402, 493-497

**N-myristoylation site.**

amino acids 173-179, 261-267, 395-401, 441-447

## **FIGURE 89**

GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCCTCTCCC GT  
CCCGCGGTGGTTGCTGCTGCCGTGCTGGCCTGAACGCAGGAGCTGTCAATTGACT  
GGCCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC TACATG  
TTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCTGGTCAT  
GTGGCTTCAGGGCGGTCCAGGC GGTCTAGCACTGGATTGGAAACTTGAGGAATTGGC  
CCCTTGACAGTGATCTAAACCACGGAAAACCACCTGGCTCCAGGCTGCCAGTCTCCTATT  
GTGGATAATCCCGTGGGCACTGGGTTCA GTTATGTGAATGGTAGTGTCCTATGCCAAGGA  
CCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGAACCTCTCAGTTGCCACAAAG  
AATTCCAGACAGTTCCATTCTACATTTCTCAGAGTCCTATGGAGGAAAATGGCAGCTGGC  
ATTGGTCTAGAGCTTATAAGGCCATT CAGCGAGGGACC ATCAAGTGCAACTTGCGGGGGT  
TGCCTTGGGTGATT CCTGGATCTCCCCTGTTGATT CGGTGCTCTCCTGGGGACCTTACCTGT  
ACAGCATGTCTCTCGAAGACAAAGGTCTGGCAGAGGTGTCAAGGTTGCAGAGCAAGTA  
CTGAATGCCGTAAATAAGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGAAAGCAGAAAT  
GATCATTGAACAGAACACAGATGGGTGAAC TTCTATAACATCTTA ACTAAAAGCACTCCCA  
CGTCTACAATGGAGTCGAGTCTAGAATT CACACAGAGCCACCTAGTTGTCTTGT CAGCGC  
CACGTGAGACACCTACAACGAGATGCCTTAAGCCAGCTCATGAATGGCCCCATCAGAAAGAA  
GCTCAAATTATT CCTGAGGATCAATCCTGGGAGGCCAGGCTACCAACGTCTTGTGAACA  
TGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATC  
AACGTGACGGTGTATAATGGACAGCTGGATCTCATCGTAGATA ACCATGGTCAGGAGGCCTG  
GGTGGAAACTGAAGTGGCAGAACTGCCTAAATT CAGTCAGCTGAAGTGGAAAGGCCCTGT  
ACAGTGACCC TAAATCTTGGAAACATCTGCTTTGTCAAGTCCTACAAGAACCTTGCTTT  
TACTGGATTCTGAAAGCTGGTCAATGGTTCTCTGACCAAGGGACATGGCTCTGAAGAT  
GATGAGACTGGTACTCAGCAAGAATAGGATGGATGGGCTGGAGATGAGCTGGTTGGCCT  
TGGGGCACAGAGCTGAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCATTCTCCCTGTATCT  
AACTGGGGCTGTGATCAAGAAGGTTCTGACCAAGCTCTGCAGAGGATAAAATCATTGTCTCT  
GGAGGCAATTGGAAATTATTCTGCTTCTTAAAAAAACCTAAGATTTTAAAAAATTGAT  
TTGTTTGATCAAAATAAGGATGATAATAGATATTAA

## FIGURE 90

MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEWDYVTVRKDAYMFWWLYYATNSC  
KNFSELPLVMWLQGGPGGSSTGFGNFEIGPLSDLKPRKTTWLQAASLLFVDNPVGTGFSY  
VNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLELYKAIQR  
GTIKCNFAGVALGDSWISPVDVSLSWGPYLYSMSLLEDKGGLAEVSKVAEQVLNAVNKGLYRE  
ATELGKAEMIIIEQNTDGVNFYNILTKSTPTSTMESLEFTQSHLVCLCQRHVRHLQRDALS  
QLMNGPIRKKLKIIIPEDQSWGGQATNVFVNMEEDFMKPVISIVDELLEAGINVTVYNGQLDL  
IVDTMGQEAWRKLKWPELPKFSQLWKALYSDPKSLETSAFKSYKNLAFYWILKAGHMVP  
SDQGDMALKMMRLVTQQE

**Signal sequence:**

amino acids 1-25

**N-glycosylation site.**

amino acids 64-68, 126-130, 362-366

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 101-105

**Casein kinase II phosphorylation site.**

amino acids 204-208, 220-224, 280-284, 284-288, 351-355, 449-453

**N-myristoylation site.**

amino acids 22-28, 76-82, 79-85, 80-86, 119-125, 169-175,  
187-193, 195-201, 331-337, 332-338, 360-366

## **FIGURE 91**

GGCCGCGGGAGAGGAGGCCATGGCGCGCGCGGGCGCTGCTGCTGGCGCTGCTGGCT  
GGGCTGGACTCAGGAAGCCGGAGTCGCAGGAGGCGGCCGTATCAGGACCATGCGGCCGA  
CGGGTCATCACGTGCGCATCGTGGGTGGAGAGGACGCCGACTGGGCGTTGGCGTGGCA  
GGGGAGCCTGCGCTGTGGATTCCCACGTATGCGGAGTGAGCCTGCTCAGCCACCGCTGGG  
CACTCACGGCGCGCACTGCTTGAAACCTATAGTGACCTTAGTGATCCCTCCGGGTGGATG  
GTCCAGTTGCCAGCTGACTTCCATGCCATCCTCTGGAGCCTGCAGGCCTACTACACCCG  
TTACTTCGTATCGAATATCTATCTGAGCCCTCGCTACCTGGGAATTCACCTATGACATTG  
CCTTGGTGAAGCTGCTGCACCTGTCACCTACACTAAACACATCCAGCCCCTGTCTCCAG  
GCCTCCACATTGAGTTGAGAACCGGACAGACTGCTGGGTGACTGGCTGGGGTACATCAA  
AGAGGATGAGGCACTGCCATCTCCCCACACCCCTCCAGGAAGGACTTCAGGTGCCATATAACA  
ACTCTATGTGCAACCACCTCTCCTCAAGTACAGTTCCGCAAGGACATCTTGGAGACATG  
GTTTGTGCTGCCAACGCCAACGGGGAGGATGCCCTGCTCGGTGACTCAGGTGGACCCCTT  
GGCCTGTAACAAGAATGGACTGTGGTATCAGATTGGAGTCGTGAGCTGGGAGTGGCTGTG  
GTCGGCCAATCGGCCGGTGTACACCAATATGCCACCACTTGAGTGGATCCAGAAG  
CTGATGGCCCAGAGTGGCATGTCCCAGCCAGACCCCTCCTGGCCACTACTCTTTCCCTCT  
TCTCTGGCTCTCCACTCCTGGGCCGGTCTGAGCCTACCTGAGCCCAGCAGCCTGGGC  
CACTGCCAAGTCAGGCCCTGGTTCTCTGTCTTGGTAATAAACACATTCCAGTTGA  
TGCCTTGCAGGGCATTCTCAAAAAAAAAAAAAAAA

## **FIGURE 92**

MGARGALLLALLLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAELGRWPWQGSLRLW  
DSHVCGVSSLHRWALTAACFETYSSDLSDPSGMVQFGQLTSMPSFWSLQAYYTRYFVSNI  
YLSPRYLGNSPYDIALVKLSAPVTYTKHIQPICLQASTFEFENRTDCWVTGWGYIKEDEALP  
SPHTLQEJVQVAIINNSMCNHLFLKYSFRKDIFGDMVCAGNAQGGKDACFGDSGGPLACNKNG  
LWYQIGVVSWVGCGRPNRPGVYTNISHHFEWIQKLMAQSGMSQPDPSWPLLFFPLLWALPL  
LGPV

**Signal sequence:**

amino acids 1-18

**N-glycosylation site.**

amino acids 167-171, 200-204, 273-277

**Casein kinase II phosphorylation site.**

amino acids 86-90, 134-138, 161-165, 190-194, 291-295

**N-myristoylation site.**

amino acids 2-8, 44-50, 101-107, 225-231, 229-235, 239-245,  
259-265, 269-275

**Amidation site.**

amino acids 33-37

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 252-263,

**Serine proteases, trypsin family, histidine active site.**

amino acids 78-84

## **FIGURE 93**

CCACCGCGTCCGGACGCGTGGGAAGGGCAGAATGGGACTCCAAGCCTGCCTCTAGGGCT  
CTTGCCCTCATCCTCTGGCAAATGCAGTTACAGCCGGAGCCGACCAGCGAGGACGC  
TGCCCCCAGGCTGGGTGTCCTGGCCGTGCGGACCCCTGAGGAAGAGCTGAGTCTCACCTT  
GCCCTGAGACAGCAGAAATGTGAAAAGACTCTCGAGCTGGTGCAGGCTGTGCGGATCCCAG  
CTCTCCTCAATAACGAAAATACCTGACCCCTAGAGAAATGTGGCTGATCTGGTGAGGCCATCCC  
CACTGACCCCTCCACACGGTGCAAAATGGCTCTGGCAGCCGGAGCCCAGAAGTGCCATTCT  
GTGATCACACAGGACTTCTGACTTGCTGGCTGAGCATCCGACAAGCAGAGCTGCTGCTCCC  
TGGGGCTGAGTTCATCACTATGTGGGAGGACCTACGGAAACCCATGTTGAAGGTCCCCAC  
ATCCCTACCAGCTTCCACAGGCCCTGGCCCCCATGTGGACTTTGTGGGGACTGCACCGT  
TTTCCCCAACATCATCCCTGAGGCAACGTCCTGAGCCGAGGTGACAGGGACTGTAGGCCT  
GCATCTGGGGTAACCCCCCTGTGATCCGTAAGCGATAACAACCTGACCTACAAGACGTGG  
GCTCTGGCACCAGCAATAACAGCCAAGCCTGTGCCAGTTCCCTGGAGCAGTATTCCATGAC  
TCAGACCTGGCTCAGTTCATGCGCTCTCGGTGGCAACTTGCACATCAGGCATCAGTAGC  
CCGTGTGGTTGGACAAACAGGGCCGGGCCGGCCGGGATTGAGGCCAGTCTAGATGTGCAGT  
ACCTGATGAGTGTGGTGCACATCTCACCTGGGCTACAGTAGCCCTGGCCGGCATGAG  
GGACAGGAGCCCTCCTGCAGTGGCTCATGCTGCTCAGTAATGAGTCAGCCCTGCCACATGT  
GCATACTGTGAGCTATGGAGATGATGAGGACTCCCTCAGCAGCGCTACATCCAGCGGTCA  
ACACTGAGCTCATGAAGGCTGCCCTGGGCTCACCCTGCTCTGCCTCAGGTGACAGT  
GGGGCCGGGTGGTCTGCTCTGGAAGACACCAGTTCCGCCCTACCTTCCCTGCCCTCCAG  
CCCCTATGTCACCACAGTGGGAGGCACATCCTCCAGGAACCTTCCATCACAAATGAAA  
TTGTTGACTATATCAGTGGTGGCTTCAGCAATGTGTTCCACGGCCTTCATACCAGGAG  
GAAGCTGTAACGAAGTCTGAGCTCTAGCCCCACCTGCCACCATCCAGTTACTTCAATGC  
CAGTGGCCGTGCCTACCCAGATGTGGCTGCACTTCTGATGGCTACTGGTGGTCAGCAACA  
GAGTGCCCATTCATGGGTGTCCGGAACCTCGGCCCTACTCCAGTGTGTTGGGGATCCTA  
TCCTGATCATGAGCACAGGATCCTTAGTGGCCGCCCCCTCTGGCTTCTCAACCCAAG  
GCTCTACCAGCAGCATGGGCAGGTCTTTGATGTAACCCGTGGCTGCCATGAGTCCTGTC  
TGGATGAAAGAGGTAGAGGGCCAGGGTTCTGCTCTGGCTGGGATCTGTAACAGGC  
TGGGGAACACCAACTTCCAGCTTGCTGAAGACTCTACTCAACCCCTGACCCCTTCTATC  
AGGAGAGATGGCTGTCCCCTGCCCTGAAGCTGGCAGTTCACTGCCTTATTCTGCCCTGTTG  
GAAGCCCTGCTGAACCCCTCAACTATTGACTGCTGCAGACAGCTTATCTCCCTAACCCGTAAA  
TGCTGTGAGCTTGACTTCAACCCCTACCATGCTCCATCATACTCAGGTCTCCCTACT  
CCTGCCCTAGATTCTCAATAAGATGCTGTAACTAGCATTTTGAAATGCCCTCTCCCTCCGC  
ATCTCATTTCTCTTCAATCAGGCTTCCAAAGGGTTGTATAACAGACTCTGTGCACTA  
TTTCACTTGATATTCACTCCCAATTCACTGCAAGGAGACCTCTACTGTCACCGTTACTCT  
TTCCTACCCCTGACATCCAGAAACAATGGCCTCCAGTGCATACTTCTCAATCTGCTTATG  
GCCTTCCATCATAGTGCCCACCTCCCTCTACTTAGCTTCAAGGTCTTAACCTCTTG  
ACTACTCTTGCTTCCCTCTCATCAATTCTGCTTCTCATGGAATGCTGACCTTCATTGC  
TCCATTGAGATTGGCTCTCAGTTACTCATTGCCCCGGAAACAAATCACTGACA  
TCTACAACCATTACCATCTCACTAAATAAGACTTTCTATCCAATAATGATTGATAACCTCAA  
TGTAAAAAA

## **FIGURE 94**

MGLQACLLGLFALILSGKCSYSPEPDQRTLPPGVSLGRADPEEELSLTFALRQQNVERLS  
ELVQAVSDPSSPQYGKYLTLENVALVRPSPLTLHTVQKWLLAAGAQKCHSVITQDFLTCWL  
SIRQAELLPGAEFHYYVGGPTETHVVRSPHPYQLPQALAPHVDFVGLHRFPPTSSLRQRP  
EPQVTGTVGLHLGVTPSVIRKRYNLTSQDVSGTSNNSQACAQFLEQYFHDSDLAQFMRLFG  
GNFAHQASVARVVGQQGRGRAGIEASLDVQYLMSAGANISTWVYSSPGRHEGQEPFLQWLML  
LSNESALPHVHTVSYGDDEDSLSAYIQRVNTELMKAARGLTLLFASGDGAGCWSVSGRH  
QFRPTFPASSPYVTTVGGTSFQEPFLITNEIVDYISGGGFSNVFPRPSYQEEAVTKFLSSSP  
HLPPSSYFNASGRAYPDVAALSDGYWVVSNRVPIPWVSGTSASTPVFGGILSLINEHRILSG  
RPPLGFLNPRLYQQHGAGLFDVTRGCHESDLDEEVEGQGFCSGPFWDPVTGWGTPTSQLC

**Signal sequence:**

amino acids 1-16

**N-glycosylation site.**

amino acids 210-214, 222-226, 286-290, 313-317, 443-447

**Glycosaminoglycan attachment site.**

amino acids 361-365, 408-412, 538-542

**Casein kinase II phosphorylation site.**

amino acids 212-216, 324-328, 392-396, 420-424, 525-529

**N-myristoylation site.**

amino acids 2-8, 107-113, 195-201, 199-205, 217-223, 219-225,  
248-254, 270-276, 284-290, 409-415, 410-416, 473-479, 482-488,  
521-527, 533-539, 549-555

## **FIGURE 95**

GCCGCGCGCTCTCTCCGGCCCCACACCTGTCTGAGCGCGCAGCGAGCCGCGGCCGGC  
GGGCTGCTCGCGCGAACAGTGCTCGGCATGGCAGGGATTCCAGGGCTCCTCTTCTC  
TTCTTCTGCTCTGTGCTGTTGGCAAGTGAGCCCTACAGTGCCCCCTGGAAACCCACTTG  
GCCTGCATAACCGCCTCCCTGTCGCTTGCCCCAGTCTACCCCTCAATTAGCCAAGCCAGACT  
TTGGAGCCGAAGCAAATTAGAAGTATCTTCTCATGTGGACCCAGTGTCTAAGGGAAC  
CCACTGCCACTTACGAAGAGGCCAAGCAATATCTGTCTTATGAAACGCTCTATGCCAATGG  
CAGCCGCACAGAGACGCAGGTGGCATCTACATCCTCAGCAGTAGTGGAGATGGGGCCAAAC  
ACCGAGACTCAGGGCTTCAGGAAAGTCTCGAAGGAAGCGGCAGATTATGGCTATGACAGC  
AGGTTCAGCATTGGAGGACTTCCTGCTCAACTACCCCTTCTCAACATCAGTGAAGTT  
ATCCACGGGCTGCACCGCACCCGGTGGCAGAGAAGCATGTCTCACAGCTGCCACTGCA  
TACACGATGAAAAACCTATGTGAAAGGAACCCAGAAGCTCGAGTGGCTCCTAAAGCCC  
AAGTTAAAGATGGTGGTCGAGGGGCCAACGACTCCACTTCAGCCATGCCGAGCAGATGAA  
ATTCAGTGGATCCGGGTGAAACGCACCCATGTGCCAAGGGTGGATCAAGGGCAATGCCA  
ATGACATCGGCATGGATTATGATTATGCCCTCTGGAACTCAAAAAGCCCCACAAGAGAAAA  
TTTATGAAGATTGGGGTGAGCCCTCTGCTAAGCAGCTGCCAGGGGCCAGGGTCTGGGTCTAT  
TGGTTATGACAATGACCGACCAGGAATTGGTGTATCGCTCTGTGACGTCAAAGACGAGA  
CCTATGACTTGCCTACCAAGCAATGCGATGCCAGCCAGGGGCCAGGGTCTGGGTCTAT  
GTGAGGATGTGGAAGAGACAGCAGCAGAAGTGGAGCGAAAAATTATTGGCATTTCAGG  
GCACCAAGTGGGTGGACATGAATGGTCCCCACAGGATTCAACGTGGCTGTCAAATCACTC  
CTCTCAAATATGCCAGATTGCTATTGGATTAAAGGAAACTACCTGGATTGTAGGGAGGG  
TGACACAGTGGTCCCTCTGGCAGCAATTAGGGCTTCATGTTCTATTAGGAGAGGCC  
AAATTGTTTTGTCAATTGGCGTGCACACGTGTGTGTGTGTGTGTAAAGGTGT  
CTTATAATCTTTACCTATTCTTACAATTGCAAGATGACTGGCTTACTATTGAAAATG  
GTTTGTGTATCATATCATATCATTAAGCAGTTGAAGGCATACTTTGCATAGAAATAA  
AAAAAAACTGATTGGGGCAATGAGGAATATTGACAATTAGTTAATCTTCACGTTTG  
CAAACTTGATTTATTCATCTGAACCTGTTCAAAGATTATTAATATTAAATATTGGCATA  
CAAGAGATATGAAAAAAAAAAAAAA

## **FIGURE 96**

MAGIPGLLFLLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLQSTLNLA  
KPDFGAEAKLEVS  
SSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRD  
SGSSGKS  
RRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTA  
AHCIHDGKTYVK  
TQKLRVGFLKPKFKDGGRGANDSTS  
SAMPEQMKFQWIRVKRTHVPKGWI  
KGANDIGMDYDYA  
LLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDV  
KDETYDLYQQCD  
AQPGASGSGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNV  
AVRITPLKYAQICYW  
IKGNYLDCREG

**Signal sequence:**

amino acids 1-19

**N-glycosylation site.**

amino acids 93-97, 207-211

**Glycosaminoglycan attachment site.**

amino acids 109-113, 316-320

**Casein kinase II phosphorylation site.**

amino acids 77-81, 95-99, 108-112, 280-284, 351-355

**N-myristoylation site.**

amino acids 159-165, 162-168, 202-208, 205-211, 314-320, 338-344

**Serine proteases, trypsin family, histidine active site.**

amino acids 171-177

## **FIGURE 97**

GCATCGCCCTGGTCTCTCGAGCCTGCTGCCGTCCCCCCCCACAGCCATGGTGGTTT  
CTGGAGCGCCCCAGCCCTGGGTGGGGCTGTCTCGCACCTCACCTCCCTGCTGCTGCTG  
GCGTCGACAGCCATCCTCAATCGGCCAGGATAACCTGTTCCCCAGCCTGTGGGAAGCCCCA  
GCAGCTGAACCGGGTTGTGGCGCGAGGACAGCACTGACAGCGAGTGGCCCTGGATCGTGA  
GCATCCAGAAGAATGGGACCCACCAC TGCGCAGGTTCTTGCTCACCA GCGCTGGGTGATC  
ACTGCTGCCACTGTTCAAGGACAACCTGAACAAACCACACCTGTTCTTGCTGCTGGG  
GGCCTGGCAGCTGGGAACCCCTGGCTCTGGTCCCAGAAGGTGGGTGTTGCCCTGGGTGGAGC  
CCCACCCCTGTGATT CCTGGAAGGAAGGTGCCTGTGCAGACATTGCCCTGGTGCCTCGAG  
CGCTCCATACAGTTCTCAGAGCGGGCCTGCCCATCTGCCTACCTGATGCCTCTATCCACCT  
CCCTCCAAACACCCACTGCTGGATCTCAGGCTGGGGAGCATCCAAGATGGAGTTCCCTTGC  
CCCACCCCTCAGACCCCTGCAGAACGCTGAAGGTTCTATCATCGACTCGGAAGTCTGCAGCCAT  
CTGTACTGGCGGGAGCAGGACAGGGACCCATCACTGAGGACATGCTGTGCGCGCTACTT  
GGAGGGGGAGCGGGATGCTGTCTGGCGACTCCGGGGCCCCCTCATGTGCCAGGTGGACG  
GCGCCTGGCTGCTGGCCGGCATCATCAGCTGGCGAGGGCTGTGCCAGCGAACAGGCC  
GGGGTCTACATCAGCCTCTTGCGCACCGCTCTGGGTGGAGAACGATCGTCAAGGGGTGCA  
GCTCCCGGGCGCGCTCAGGGGGTGGGCCCTCAGGGCACCGAGCCAGGGCTCTGGGCCG  
CCGCGCGCTCCTAGGGCGCAGCGGACCGGGCTCGGATCTGAAAGGCGCCAGATCCACA  
TCTGGATCTGGATCTGCGCGGCCCTCGGCGGTTCCCCCGCCGTAAATAGGCTCATCTACC  
TCTACCTCTGGGGGCCGGACGGCTGCTGCGGAAGGAAACCCCTCCCCGACCCGCCGAC  
GGCCTCAGGCCCCCTCCAAGGCATCAGGCCCGCCAACGGCCTCATGTCCCCGCCAAC  
GACTTCCGGCCCCGCCCCCGAGCGCTTTGTGTATATAATGTTAATGATTTTAT  
AGGTATTTGTAACCCCTGCCACATATCTTATTATTCTCCAATTCAATAATTATTATT  
CTCCAAAAAAA

## **FIGURE 98**

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA43318  
><subunit 1 of 1, 317 aa, 1 stop  
><MW: 33732, pI: 7.90, NX(S/T): 1  
MVVSGAPPALGGGCLGTFTSLLLLASTAILNAARI PVPPACGKPQQLNRVVGGEDSTDSEWP  
WIVSIQKNGTHHCAGSLLTSRWVITAHCFKDNLNKPYLFSVLLGAWQLGNPGSRSQKVGVA  
WVEPHPVYSWKEGACADIALVRLERSIQFSERVLPICL PDASIHLPPNTHCWISGWGSIQDG  
VPLPHPQTLQKLKVPIIDSEVC SHLYWRGAGQGPITEDMLCAGYLEGERDACLGDGGPLMC  
QVDGAWLLAGIISWGEGCAERNRPGVYISLSAHRSWEKIVQGVQLRGRAQGGGALRAP SQG  
SGAAARS

**Signal sequence:**

amino acids 1-32

**N-glycosylation site.**

amino acids 62-66, 96-100, 214-218, 382-386, 409-413, 455-459,  
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

**Glycosaminoglycan attachment site.**

amino acids 826-830

**Casein kinase II phosphorylation site.**

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,  
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,  
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,  
1013-1017, 1019-1023, 1021-1025

**Tyrosine kinase phosphorylation site.**

amino acids 607-615

**N-myristoylation site.**

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,  
612-618, 623-629, 714-720, 873-879

## **FIGURE 99**

GACGGCTGGCCACCATGCACGGCTCTGCAGTTCTGATGCTTCTGCTGCCGCTACTGCTA  
CTGCTGGTGGCCACCACAGGCCCGTTGGAGCCCTCACAGATGAGGAGAACGTTGATGGT  
GGAGCTGCACAACCTCTACCGGGCCCAGGTATCCCCGACGGCCTCAGACATGCTGCACATGA  
GATGGGACGAGGAGCTGGCCGCTTCGCCAAGGCCTACGCACGGCAGTGCCTGTGGGCCAC  
AACAAAGGAGCGCGGGCGCCGCGCGAGAAATCTGTTGCCATCACAGACGAGGGCATGGACGT  
GCCGCTGGCCATGGAGGAGTGGCACCACGAGCGTGAGCACTACAACTCAGGCCGCCACCT  
GCAGCCCAGGCCAGATGTGCGGCCACTACACGCAGGTGGTATGGCCAAGACAGAGAGGATC  
GGCTGTGGTCCCACCTCTGTGAGAAGCTCCAGGGTGTGAGGAGACCAACATCGAATTACT  
GGTGTGCAACTATGAGCCTCCGGGAACGTGAAGGGAAACGCCCTACCAGGAGGGACTC  
CGTGCTCCCAATGTCCCTCTGGCTACCACTGCAAGAACTCCCTCTGTGAACCCATCGGAAGC  
CCGGAAGATGCTCAGGATTGCCCTACCTGGTAAC TGAGGCCCATCCTTCCGGCGACTGA  
AGCATCAGACTCTAGGAAAATGGGTACTCCTTCCCTAGCAACGGGATTCCGGCTTCT  
TGGTAACAGAGGTCTCAGGCTCCCTGGCAACCAAGGCTCGCCTGCTGTGAAACCCAGGCC  
CCAACCTCCTTAGCAACGAAAGACCCGCCCTCCATGGCAACAGAGGCTCCACCTGCGTAAC  
AACTGAGGTCCCTCATTGGCAGCTCACAGCCTGCCCTGGATGAGGAGCCAGTTA  
CCTTCCCCAAATCGACCCATGTTCTATCCAAAATCAGCAGACAAAGTGACAGACAAAACA  
AAAGTGCCCTCTAGGAGCCCAGAGAACTCTCTGGACCCCAAGATGTCCTGACAGGGCAAG  
GGAACCTCCTACCCATGCCAGGAGGAGGCTGAGGCTGAGGCTGAGTTGCCCTCCAGTG  
AGGTCTTGGCCTCAGTTTCCAGGCCAGGACAAGCCAGGTGAGCTGCAGGCCACACTGGAC  
CACACGGGGCACACCTCCTCCAAGTCCCTGCCAATTCCCCAATACCTCTGCCACCGCTAA  
TGCCACGGGTGGCGTGCCTGGCTCTGAGTCGCTGCCAGGTGCAGAGGCCCTGACA  
AGCCTAGCGTTGTGTCAGGGCTGAACCTGGCCCTGGTCACTGTGTTGGCCCTCTGGGA  
CTACTGCTCCTGCCTCCTCTGGTGTGGCTGGAATCTCTTGAATGGATACCACTCAAAGGG  
TGAAGAGGTAGCTGTCCTCTGTCACTTCCCCACCCCTGTCCCCAGCCCTAAACAAGATA  
CTTCTTGGTTAAGGCCCTCGGAAGGGAAAGGCTACGGGCATGTGCCTCATCACACCATCC  
ATCCTGGAGGCACAAGGCCTGGCTGGCTGCGAGCTCAGGAGGCCCTGAGGACTGCACACC  
GGGCCACACCTCTCCTGCCCTCCCTCCTGAGTCCTGGGGTGGGAGGATTGAGGGAGCT  
CACTGCCTACCTGGCCTGGGCTGTCTGCCACACAGCATGTGCCTCTCCCTGAGTGCCTG  
TGTAGCTGGGATGGGATTCCCTAGGGCAGATGAAGGACAAGCCCCACTGGAGTGGGTTTC  
TTTGAATGGGGAGGCAGGGACGGAGGAAGGAAAGTAACCTGACTCTCCAATAAAACCT  
GTCCAACCTGTGAAA

## **FIGURE 100**

MHGSCSFLMLLLPLLLLLVATTGPVGALTDEEKRLMVELHNLYRAQVSPTASDMLHMRWDEE  
LAAFAKAYARQCVGHNKERGRGENLFAITDEGMDVPLAMEEWHHEREHYNLSAATCSPGQ  
MCGHYTQVVWAKTERIGCGSHFCEKLQGVEETNIELLVCNYEPPGNVKGKRPYQEGETPCSQC  
PSGYHCKNSLCEPIGSPEDAQDLPYLVTEAPSFRATEASDSRKMGTPSSLATGIPAFLVTEV  
SGSLATKALPAVETQAPTSLATKDPPSMATEAPPCVTTEVPSILAHSPLSLDEEPVTFPKS  
THVPIPKSADKVTDKTKVPSRSPENSLDPKMSLTGARELLPHAQEEAEAAELPPSSEVLAS  
VFPAQDKPGELQATLDHTGHTSSKSLPNFPNTSATANATGGRALALQSSLPGAEGPDKPSVV  
SGLNSGPGHVWGPLLGLLLLPLVLAGIF

**Signal sequence:**

amino acids 1-22

**N-glycosylation site.**

amino acids 114-118, 403-407, 409-413

**Glycosaminoglycan attachment site.**

amino acids 439-443

**Casein kinase II phosphorylation site.**

amino acids 29-33, 50-54, 156-160, 195-199, 202-206, 299-303

**N-myristoylation site.**

amino acids 123-129, 143-149, 152-158, 169-175, 180-186, 231-237,  
250-256

**Amidation site.**

amino acids 82-86, 172-176

**Peroxidases proximal heme-ligand signature.**

amino acids 287-298

**Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1.**

amino acids 127-138

**Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2.**

amino acids 160-172

## **FIGURE 101**

GTAACGTAGGCTTTCATTGGAGCCCCCAACAGAACCGTCATTCTCCAAGTTATGGTGGACGT  
ACTCTGTTCTCCCTGCTTGCTTTCACATTAGCAGACCGACTAAGTCACAACAGATTATCTTCAT  
CAAGGCAAGTCCATGAGCCACCTCAAAGCCTCGAGAAAGTGAACAAACAAATGAATTGGAGACCATTCC  
AAATCTGGGACCAAGTCTGGCAAATATTACACTCTCTCCTGGCTGAAACAGGATTGTGAAATACCTCCCTGA  
ACATCTGAAAGAGTTCACTGCCCTGAAACTTGGACCTTAGCAGCAACAATATTTCAGAGCTCCAAACTGCATT  
TCCAGCCCTACAGCTAAATATCTGTATCTCACAGCAACCGACTCACATCAATGGAACCTGGTATTGGACAA  
TTTGGCCAACACACTCCTGTGAAAGCTGAACAGGAACCGAATCTCAGCTATCCCACCCAAGATGTTAAACT  
GCCCAACTGCAACATCTGAATTGAACCGAAACAAGATTAAGATGGACTGACATTCCAAGGCCCTGG  
TGCTCTGAACTCTGAAATGCAAAGAAATGGAGTAACGAAACTTATGGATGGACTTTTGGGGCTGAGCAA  
CATGGAAATTTCAGCTGGACATAACACCTAACAGAGATTACCAAAGGCTGGCTTACGGCTTGCTGATGCT  
GCAGGAACCTCATCTCAGCCAAATGCCATCACAGGATCAGCCCTGATGCCCTGGAGTTCTGCCAGAAGCTCAG  
TGAGCTGGACCTAATTCAATCACTTATCAAGGTTAGATGATTCAAGCTTCTGGCTAAGCTTACTAAATAC  
ACTGCACATTGGAAACAACAGAGTCAGCTACATTGCTGATTGCTCTCCGGGGCTTCCAGTTAAAGACTTT  
GGATCTGAAAGACAATGAAATTCTGGACTATTGAAGACATGAATGGCTTCTGGAGTTGACAAACTGAG  
GCGACTGATACTCCAAGGAAATCGGATCCGTTCTATTACTAAAAAGCTTCACTGGTTGGATGATTGGAGCA  
TCTAGACCTGAGTGAACCGCAATCATGCTTTACAAGGCAATGCATTTCACAAATGAAGAAACTGCAACAATT  
GCATTAAATACATCAAGCCTTTGTGCATTGCCAGCTAAATGGCTCCACAGTGGTGGCGAAAACAACCTT  
TCAGAGCTTGTAAATGCCAGTTGTGCCTCAGCTGCTAAAGGAAGAACGATTGGCTGTTAGGCCAGA  
TGGCTTGTGTGATGATTCCCAAACCCAGATCACGGTTAGCCAGGAAACACAGTCGGCAATAAAAGGTT  
CAATTGAGTTCATCTGCTCAGCTGCCAGCAGCTGATCCCAATGACTTTGCTTGGAAAAAAAGACAATGA  
ACTACTGCATGATGCTGAAATGAAATTATGCACACCTCCGGGCCAAGGTGGCAGGTGATGGAGTATACCAC  
CATCCTCGGCTGCGGAGGTGAAATTGCCAGTGAGGGAAATATCAGTGTGTCATCTCAATCACTTGGTC  
ATCCTACTCTGCAAAGCCAAGCTTACAGTAAATATGCTTCCCTCATTCAACAGACCCCCATGGATCTCACC  
CCGAGCTGGGGCCATGGCACGCTTGGAGTGTGCTGTGGGACCCAGCCCCCAGATAGCCTGGCAGAAGGA  
TGGGGCACAGACTTCCAGCTGCACGGAGAGACGATGCATGTGATGCCAGGTGAGTGTCTTATCGT  
GGATGTGAAAGATAGAGGACATTGGGTATACAGCTGCACAGCTCAGAACAGTGCAGGAAGTATTCAGCAAATGC  
AACTCTGACTGTCTAGAAACACCATCATTTTGCGGCCACTGTTGGACCGAACGTGTAACCAAGGGAGAAACAGC  
CGTCCTACAGTCATTGCTGGAGGAAGGCCCTCCCCCTAAACTGAACTGGACCAAAGATGATAGCCCATTGGGGT  
AACCGAGAGGCACTTTTGCAAGGCAATCAGCTCTGATTATTGTGGACTCAGATGTGATGCCAGGTGAG  
ATACACATGTGAGATGCTAACACCCCTGGCACTGAGAGGAAACCTGGCCTCAGTGTGATCCCCACTCCAAC  
CTGCGACTCCCCCTCAGATGACAGCCCCATGTTAGACGATGACGGATGGGCACTGTGGTGTGATCATAGC  
CGTGGTTGCTGTGGTGGCACGTCACTCGTGTGGTGTGATCATATACACACAAGGGGAGGAATGAAGA  
TTGCAGCATTACCAACACAGATGAGACCAACTGCCAGCAGATATTCTAGTTATGTGATCTCAGGGAACGTT  
AGCTGACAGGCAGGATGGGTACGTGCTTCAGAAAGTGGAGGCCACCCAGTTGTCACATCTCAGGTGCTGG  
ATTTTCTTACACACATGACAGTAGTGGACCTGCCATTGACAATAGCAGTGAAGCTGATGTGGAGCTGC  
CACAGATCTGTTCTTGTCCGTTTGGGATCCACAGGCCCTATGTATTGAAAGGGAAATGTGATGGCTCAGA  
TCCTTTGAAACATATCATACAGGTTGCACTGCTGACCCAAAGAACAGTTTATGGACCACTATGAGCCCAGTT  
CATAAAGAAAAGGAGTGCACCCATGTTCTCATCCTTCAGAAGAACCTGCGAACGGAGCTCAGTAATATATC  
GTGGCTTCACATGTGAGGAAGCTACTTAACACTAGTTACTCTCACAAATGAAGGACCTGGAATGAAAATCTGT  
TCTAAACAAGTCTCTTGTGAAAGCTCATTCTCCAGACTTGGACTCTGGGTGAGGAAATGGCTCAGAG  
AAGGCCCTTATTGAAAGCTCATTCTCCAGACTTGGACTCTGGGTGAGGAAAGATGGGAAAGAAAGGAC  
AGATTTCAGGAAGAAAATCACATTGTACCTTAAACAGACTTTAGAAAACAGACTCCAAATTTCAGTC  
TTATGACTTGGACACATAGACTGAATGAGACCAAAGGAAAAGCTTAACATACTACCTCAAGTGAACCTTATT  
AAAGAGAGAGAAATCTTATGTTTAAATGGAGTTATGAATTAAAAGGATAAAAATGCTTTATTATACAGAT  
GAACCAAAATTACAAAAAGTTATGAAAATTGAGTTACTGGGAATGATGCTCATATAAGAACACCTTTAAACTA  
TTTTTTAACTTGTGTTATGCAAAAAGTATCTACGTAATTAAATGATATAAAATCATGATTATTGATGTT  
TTATAATGCCAGATTCTTTATGAAAATGAGTTACTAAAGCATTAAATAACCTGCCCTGTACCACTT  
TTAAATAGAAGTTACTCATTATATTGACATTATTTAATAAAATGTGTCACATTGAA

## **FIGURE 102**

MVDVLLFSLCLLFHISRPDLSHNRLSFIKASSMSHLQLSQLREVKLNNNELETIPNLGPVSAN  
ITLLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVTSMEP  
GYFDNLANTLLVLKLNRRNRIASIPPKMFKLPQLQHLELRNKIKNVGLTFQGLGALKSLKM  
QRNGVTKLMGAFWGLSNMEILQLDHNNLTEITKGWLYGLLMLQELHLSQNAIRISPDAWE  
FCQKLSELDLTFNHLRSRLLDDSSFLGLSLLNTLHIGNNRVSYIADCAFRLSSLKTLDDLKNNE  
ISWTIEDMNGAFSGLDKLRRLILQGNRIRSITKKAFTGLDALEHLDLSDNAIMSLQGNAFSQ  
MKKLIQQLHLNTSSLLCDCQLKWLPOWVAENNQSFVNASCAPQLLKGRSIFAVSPDFVCD  
DFPKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKDNELLHDAEMENYAHLRQAQG  
GEVMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTVNMLPSFTKTPMDLTIRAGA  
MARLECAAVGHPAPQIAWQKDGGTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCAQN  
SAGSISANATLTVLETPSFLRPLLDRTVTKGETAVLQCIAGGSPPPKNWTKDDSPVVTER  
HFFAAGNQLLIIVDSDVSDAGKYTCEMSNTLGTERGNVRLSVIPTPTCDSPQMTAPSLLDDG  
WATVGVIIIAVVCCVVGTSLVVVVIYHTRRRNEDCSITNTDETNLPADIPSYLSSQGTTLAD  
RQDGYVSSESGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEAATDLCFLCPFLGSTGP  
MYLKGNVYGSDPFETYHTGCPDPRTVLMHYEPSYIKKKECYPCHPSEESCRFSNISW  
PSHVRKLLNTSYSHNEGPGMKNLCLNKSSLDFSANPEPASVASSNSFMGTFGKALRRPHLDA  
YSSFGQPSDCQPRAFYLAHSSPDLDGSEEDGKERTDFQEENHICTFKQTLENYRTPNFQS  
YDLDT

**Signal sequence:**

amino acids 1-19

**Transmembrane domain:**

amino acids 746-765

**N-glycosylation site.**

amino acids 62-66, 96-100, 214-220, 382-386, 409-413, 455-459,  
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

**Glycosaminoglycan attachment site.**

amino acids 826-830

**Casein kinase II phosphorylation site.**

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,  
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,  
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,  
1013-1017, 1019-1023, 1021-1025

**Tyrosine kinase phosphorylation site.**

amino acids 607-615

**N-myristoylation site.**

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,  
612-618, 623-629, 714-720, 873-879

## **FIGURE 103**

GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTGGTGGTGGCTTGGGTGCCTGCAAAATG  
AAGGATGCAGGACGCAGCTTCTCCTGGAACCGAACGCAATGGATAAACTGATTGTGCAAGAGAGAAGAAC  
GAAGCTTTCTTGTGAGCCCTGGATCTAACACAAATGTGTATATGTGCACACAGGGAGCATTCAAGAATGAAA  
TAAACCAGAGTTAGACCCCGGGGGTGGTGTCTGACATAAATAATCTTAAAGCAGCTGTTCCCTCC  
CCACCCCCAAAAAAAGGATGATTGAAAGAACGAGGATTCAAAGAAAAAGTATGTTCATTTCTC  
TATAAAGGAGAAAGTGAACGCCAAGGGAGATATTGGAATGAAAAGTTGGGGCTTTTAGTAAAGTAAGAACT  
GGTGTGGTGGTGTCTTCTTGAATTCCCACAAAGAGGAGAGGAAATTAAATAACATCTGCAAAGAAA  
TTTCAGAGAAGAAAAGTGAACCGCAGATTGAGGCATTGATTGGGGAGAGAAACACAGCAGAGCACAGTTGGA  
TTTGTGCCTATGTTGACTAAAATTGACGGATAATTGCACTGGATTCTCTTCTTCAACCTCCATTTTTAAAT  
TTTTATTCCCTTTGGTATCAAGATCATGCCTTCTCTTCTTCAACACCCTGGATTCCATCTGGATGTTGCT  
GTGATCAGTCTGAAATACAACACTGTTGAATTCCAGAACGGACAAACACAGATAAATTGAAATGTTGAAACAAGAT  
GACCTTACATCCACAGCAGATAATGATAGGTCTAGGTTAACAGGGCCCTATTGACCCCTGCTTGCTGGTCT  
GCTGGCTCTCAACTCTTGTGGTGGCTGGTCTGGTGGCTCAGACACTGCCCTCTGTGCTCTGGAGCAA  
CCAGTTCAAGGTGATTGTTGGAAAAACCTCGTGGAGGTTCCGGATGGCATCTCCACCAACACAGGCT  
GCTGAACCTCCATGAGAACCAAATCCAGATCATCAAAGTGAACAGCTCAAGCACTTGAGGACTTGGAAATCCT  
ACAGTTGAGTAGGAACCATATCAGAACCAATTGAAATTGGGGCTTCAATGGTCTGGGAACCTCAACACTCTGGA  
ACTCTTGACAATCGTCTACTACCATCCGAATGGAGCTTTGTATCTGTCTAAACTGAAGGAGCTCTGGTT  
GCGAAACAACCCATTGAAAGCATCCCTCTTACAGAATTCCCTTGCCTGGACTAGACTTAGG  
GGAATTGAAAAGACTTTCATACATCTCAGAAGGTGCTTGAAGGTCTGCCAACCTGAGGATTGAAACCTTGC  
CATGTGCAACCTCGGGAAATCCCTAACCTCACACCGCTCATAAAACATAGATGAGCTGGATCTTCTGGGAATCA  
TTTATCTGCCATCAGGCCTGGCTCTTCCAGGGTTGATGCACCTTCAAAACTGTGGATGATACTGCTCCAGAT  
TCAAGTGAACGGAATGCCCTTGACAACCTCAGTCACTAGTGGAGATCAACCTGGCACACAATACTAAC  
ATTACTGCCTCATGACCTCTCACTCCCTTGACATCATCTAGAGCGGATACATTACATACAACCCCTGGAACTG  
TAACTGTGACATACTGTGGCTCAGCTGGTGGATAAAAGACATGGCCCTCGAACACAGCTTGTGCCCCGGTG  
TAACACTCCTCCAACTCAAAGGGGAGGTACATGGAGAGCTGACCAGAAATTACTCACATGCTATGCTCCGGT  
GATTGGAGCCCCCTGCAGACCTCAATGTCAGTAAGGCATGGCAGCTGAGCTGAAATGTCGGGCTCCACATC  
CCTGACATCTGTATCTGGATTACTCCTAACATGGAACACTCATGACACATGGGGCTACAAAGTGGATAGCTGT  
GCTCAGTGTGGTACGTTAAATTTCACAAATGTAACGTGCAAGATAAGGCATGTACACATGTTGAGTAA  
TTCCGGTGGGAATACTACTGCTTCAGGCACCCCTGAATGTGTTACTGAGCAAGGACTACTCCTTCTTACTTTTCA  
AACCGTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGCACGGACACAGATAACAATGTCGGGCTCCACTCC  
AGTGGTCGACTGGAGACCAATGTGACCACTCTCTCACACCACAGAGCACAAGGTCGACAGAGAAAAACCTT  
CACCATCCCAGTGAATGATATAAACAGTGGGATCCCAGGAATTGATGAGGTCTGACAGACTACCAAAATCATCAT  
TGGGTGTTTGTGGCCATCACACTCATGGCTGAGTGTGGTCTTACAAAGATGAGGAAGCAGCACCA  
TCGGCAAAACCATCACGCCAACAAAGGACTGTGAAATTATTAATGTGGATGAGATTACGGGAGACACACC  
CATGGAAAGGCCACCTGCCATGCCTGCTATCGAGCATGAGGCACCTAAATCACTATAACTCATACAAATCTCCCTT  
CAACCACACAACACAGTTAACACAATAATTCAATACACAGTTCACTGAGTGAACCGTTATTGATCCGAATGAA  
CTCTAAAGACAATGTACAAGAGACTCAAATCTAAACACTGAGTTACAAAAACAAACAAATCAAAAAAA  
GACAGTTATTAAAAATGACACAAATGACTGGGCTAAATCTACTGTTCAAAAGTGTCTTACAAAAACAA  
AAAAGAAAAGAATTATTATTAAAAATTCTATTGTGATCTAAAGCAGACAAAAAA

## **FIGURE 104**

MLNKMTLHPQQIMIGPRFNRALFDPLLVVLLALQLLVVAGLVRAQTCPSVCSCSNQFSKVIC  
VRKNLREVPDGISTNTRLLNLHENQIQIICKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLA  
NLNTLELFNDNRLTTIPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLS  
YISEGAFEGLSNLRYLNLCNLREIPNLTPLIKLDELDLSGNHLSAIRPGSFQGLMHLQKL  
WMIQSQIQVIERNADFNLQSLVEINLAHNNLTLLPHDLFTPPLHHLERIHLHHNPWCNC  
WLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNTEGMAAE  
LKCRASTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVQDTGMYTCMVNSVGN  
TTASATLNVTAATTPFSYFSTVTVETMEPSQDEARTTDNNVGPTPVVDWE  
TTNVTTSLTPQSTRSTEKTFTIPVTDINSGIPGIDEVMKTTKIIIGCFVAITLMAAVMLVIFYKMRKQHHRQN  
HHAPTRTVEIINV  
DDEITGDTPMESHLPM  
PAIEHEHLHYNSYKSPFNHTT  
TVNTINSIHSS  
VHEPLLIR  
MNSKDNVQETQI

**Signal sequence:**

amino acids 1-44

**Transmembrane domain:**

amino acids 523-543

**N-glycosylation site.**

amino acids 278-282, 364-368, 390-394, 412-416, 415-419, 434-438,  
442-446, 488-492, 606-610

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 183-187

**Casein kinase II phosphorylation site.**

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

**N-myristoylation site.**

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,  
391-397, 422-428, 433-439, 531-537

## **FIGURE 105**

AGCCGACGCTGCTCAAGCTGCAACTCTGTCAGTTGCAGTTGGCAGTTCTTCCGTTCCCTGCTGTTGGGGCA  
TGAAAGGGCTTCGCCGCCGGAGTAAAAGAAGGAATTGACCAGGGCAGCGCAGGGAGGAGCGCAGCGACCGC  
GAGGGCGGGCGTGCACCCCTCGGCTGAAAGTTGTGCCGGGCCCCGAGCGCGCCGCGCTGGAGCTTCGGTAGA  
GACCTAGGCCGCTGGACCGCGATGAGCGCAGCGCAGCCTCCGTGCGCGCCGCGGGTTGGGCTGCTGCTGTG  
GCGGTGCTGGGGCGCTGGCGCTGGACAGCGCGGGTCCGAGCAGCGCGGGACTCGGGAGCCCTCTGGGTAGCGCC  
GAGCGCCCATGCCCACTACCTGCCCTGCCCTGGGGACCTGCTGGACTGCACTGTAAGCGGCTAGCGCTT  
CCCCAGCCACTCCCGTCTGGGTGCGCTGGACTTAAGTCACAACAGATTATCTTCATCAAGGCAAGTTCC  
ATGAGCCACCTCAAAGCCTCGAGAAGTGAAGACTGAACACAATGAATTGGAGAACATTCCAATCTGGGACCA  
GTCTGGCAAATTACACTTCTCTTGGCTGAAACAGGATTGTGAAACTACCTCTGAACATCTGAAAGAG  
TTTCAGTCCCTGAAACTTGGACCTTAGCAGCAACAAATTTAGAGCTCAAACAGCATTCCAGCATTCCAGC  
CTCAAATATCTGTATCTCAACAGCAACCGAGTCACATCAATGGAACCTGGGTATTGACAATTGGCCAACACA  
CTCCTGTGTTAAAGCTGAACAGGAACCGAATCTCAGCTATCCCACCCAAAGATGTTAAACTGCCCAACTGCAA  
CATCTGAATTGAAACGAAACAAGATTAAAGTAGATGGACTGACATTCAACAGGCTTGGTGTCTGAAGTCT  
CTGAAAATGCAAGAAATGGAGTAACGAAACTTATGGATGGAGCTTTTGGGGCTGAGCAACATGAAATTG  
CAGCTGGACCATAACACCTAACAGAGATTACCAAAGGCTGGCTTACGGCTTGTGATGCTGAGGAACATT  
CTCAGCCAAATGCCATCAACAGGATCAGCCCTGATGCCCTGGAGTTCTGCCAGAAGCTCAGTGAGCTGGACCTA  
ACTTTCAATCACTTCAAGGTTAGATGATTCAAGCTTCTGGCTAAGCTTACTAAATACTGCACATTGGG  
AACAAACAGAGTCAGCTACATTGCTGATTGTGCCCTCCGGGGCTTCCAGTTAAAGACTTGGATCTGAAGAAC  
AATGAAATTCTGGACTATTGAAGACATGAATGGTCTTCTCTGGGCTTGACAACACTGAGGCGACTGATACTC  
CAAGGAAATCGGATCCGTTCTATTACTAAAAAGCCTTCACTGGTTGGATGCAATTGGAGCATCTAGACCTGAGT  
GACAACGCAATCATGCTTTACAAGGCAATGCATTTCACAAATGAAGAAACTGCAACAATTGCAATTAAATACA  
TCAAGCCTTTGTGCAATTGCCAGCTAAATGGCTCCCACAGTGGGGCGGAAACAAACTTCAAGAGCTTGT  
AATGCCAGTTGCCATTCTCAGCTGCTAAAGGAAGAACGATTGGCTGTTAGCCAGATGGCTTGT  
GATGATTTCACAAACCCAGATCACGGTTCAGGCCAGAAACACAGTCGGCAATAAAGGTTCCAATTGAGTT  
ATCTGCTCAGCTGCCAGCAGCAGTGATTCCCCAATGACTTTGCTGGAAAAAGACAATGAACTACTGC  
GCTGAAATGGAAAATTATGCAACACCTCCGGGCCAAGGTGGCAGGTGATGGAGTATACCAACCATCTTGGCTG  
CGCAGGGTGGAAATTGCCAGTGAGGGAAATATCAGTGTGTCATCTCCAATCAGTGTGTTCATCCTACTCTG  
AAAGCCAAGCTTACAGTAATATGCTTCCCTATTCCAAAGACCCCCATGGATCTCAGGAGCTGGGGCC  
ATGGCACGCTGGAGGTGTGCTGCTGGGGCACCCAGCCCCCAGATGCGTGGAGAAGGATGGGGCACAGAC  
TTCCCAGCTGACGGAGAGACGATGATGTCAGTGTGATGCCAGGGATGACGTGTTCTTATCGTGGATGT  
GAGGACATTGGGTATACAGCTGCACAGCTCAGAACAGTGCAAGGAGTATTGCAAAATGCAACTCTGACTG  
CTAGAAACACCATCATTTGCGGCCACTGTTGGACCGAACTGTAACCAAGGGAGAACAGCCGCTTACAGTGC  
ATTGCTGGAGGAAGGCCCTCCCCCTAAACTGAACCTGGACCAAAGATGATGAGCCATTGGTGGTAACCGAGAGGC  
TTTTTGCAAGCAGGAATCAGCTCTGATTATTGGAACCTCAGATGTCAGTGCTGGAAATACACATGTGAG  
ATGCTAACACCTTGGCACTGAGAGAGGAAACGTCAGGCCACTCCAAACCTGCACTCCCCT  
CAGATGACAGCCCCATCGTTAGACGATGACGGATGGGCCACTGTGGGTGCTGATCATAGCCGTGGTTGCTGT  
GTGGGGCACGTCACTCGTGTGGGTGATCATATAACCACACAAGCGGAGGAATGAAGATTGCAAGCATTAC  
AACACAGATGAGACCAACTTGCACAGATATTCTAGTTATTGTCATCTCAGGAAACGTTAGCTGACAGGAG  
GATGGGTACGTTGCTTCAAGAAAGTGAAGGCCACCCAGTTGTCACATCTCAGGTGCTGGATTTCCTTACCA  
CAACATGACAGTAGTGGCACCTGCCATTGACAATAGCAGTGAAGCTGATGTGAGCTGCCACAGATCTGTT  
CTTGTGCGTTGGGATCCCACAGGCCCTATGTTAGGGAAATGTGTATGGCTCAGATCTTGGAAACA  
TATCATACAGGTTGCACTCCTGACCCAGAAACAGTTTAATGGACCACTATGAGCCAGTTACATAAAGAAAAG  
GAGTGTACCCATGTTCTCATCCTCAGAAGAACTCTGCAACGGAGGCTTCAGTAATATATCGTGGCTTCACAT  
GTGAGGAAGCTTAACACTAGTTACTCTCACAAATGAAGGACCTGGAAATGAAAATCTGTCATAAACAGTCC  
TCTTGTGTTTAATGGAGTTATGAAATTAAAAGGATAAAATGCTTATTATACAGATGAAACCAAAATTAC  
AAAAAGTTATGAAATTTTATACTGGGAATGATGCTCATATAAGAATACCTTTAAACTATTTTAACTTT  
TTTATGCAAAAAGTATCTACGTTAAATTAAATGATATAATCATGATTATTTATGTTATTTATAATGCCAGA  
TTTCTTTATGGAAATGAGTTACTAAAGCATTAAATAACCTGCCCTGTGACCAATTAAATAGAAGTT  
ACTTCATTATATTTGCACATTATTTAAATAATGTGCAATTGAAAAA

## **FIGURE 106**

MSAPSLRARAAGLGLLLCAVLGRAGRSDSGGRGELGQPSGVAEERPCPTTCRCLGDILLDCSR  
KRLARLPEPLPSWVARLDLSHNRLSFIKASSMSHLQSLREVKLNNELETIPNLGPVSANIT  
LLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVTSMEPGY  
FDNLANTLLVLKLNRNRISSAIPPKMFKLPQLQHLELNRNKIKNVGGLTFQGLGALKSLKMQR  
NGVTKLMDGAFWGLSNMELQLDHNNLTEITKGWLGYGLLMLQELHLSQNAINRISPDAWEFC  
QKLSELDLTFTNHLRSRLLDDSSFLGLSLLNTLHIGNNRVSYIADCAFRLGSSLKTLKLNNEIS  
WTIEDMNGAFSGLDKLRRLILQGNRIRSITKKAFTGLDALEHLDLSDNAIMSLQGNAFSQMK  
KLQQLHLNTSSLCDQLKWLPOWVAENNFQSFVNASCAPHQPLLKGRSIFAVSPDGVCDDF  
PKPQITVQPETQSAIKGSNLNFICSAASSSDSPMTFAWKKDNELLHDAEMENYAHLRAQGE  
VMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTVNMLPSFTKTPMDLTIRAGAMA  
RLECAAVGHPPAQIAWQKDGGTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCTAQNSA  
GSISANATLTVLETPSFLRPLLDRVTKGETAVLQCIAGGSPPPKNWTKDDSPLVVTERHF  
FAAGNQLLIIVDSDVSDAGKYTCEMSNTLGERGNVRSLVIPTPTCDSPQMTAPSLLDDGWA  
TVGVVIIAVVCCVVGTSLVVVIIYHTRRRNEDCSITNTDETNLPADIPSYLSSQGTLADRO  
DGYVSSESQSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEAATDLFLCPFLGSTGPMY  
LKGNVYGSDFPFETYHTGSPDPRTVLMHYEPSYIKKKECYPCHPSEESCRSFSNISWPS  
HVRKLLNTSYSYSHNEGPGMKNLCLNKSSLDFSANPEPASVASSNSFMGTFGKALRRPHLDAYS  
SFGQPSDCQPRAFYLKAHSSPDLDGSEEDGKERTDFQEENHICTFKQTLNEYRTPNFQSYDLDT

**Signal sequence:**

amino acids 1-27

**Transmembrane domain:**

amino acids 808-828

**N-glycosylation site.**

amino acids 122-126, 156-160, 274-278, 442-446, 469-473, 515-519,  
688-692, 729-733, 905-909, 987-991, 999-1003, 1016-1020

**Glycosaminoglycan attachment site.**

amino acids 886-890

**Casein kinase II phosphorylation site.**

amino acids 99-103, 180-184, 263-267, 314-318, 324-328, 374-378,  
383-387, 407-411, 524-528, 608-612, 692-696, 709-713, 731-735,  
799-803, 843-847, 863-867, 907-911, 1003-1007, 1018-1022,  
1073-1077, 1079-1083, 1081-1085

**Tyrosine kinase phosphorylation site.**

amino acids 667-675

**N-myristoylation site.**

amino acids 14-20, 36-42, 239-245, 257-263, 380-386, 427-433,  
513-519, 588-594, 672-678, 683-687, 774-780, 933-939

**Leucine zipper pattern.**

amino acids 58-80, 65-87

## **FIGURE 107**

CAAAACTTGCCTCGCGGAGAGCGCCCAAGCTTGAATGGAAGGAGCCCAGGCCGGAGCGCAGCTGAGAC  
TGGGGGAGCGCGTTGGCCCTGTGGGCGCCGCTCGGCGCCGGGCGCAGCAGGGAAAGGGAGCTGTGGTCTGCC  
CTGCTCCACGAGGCAGCCACTGGTGTGAACCGGGAGAGGCCCTGGGTGTCCTCCCTATCCCTCCTTATATA  
GAAACCTTCCACACTGGGAAGGGAGCCGGCAGGGCAGGGCTCATGGTGAAGCAAGGAGGCCGGCTGATCTGCAG  
GCGCACAGCATTGGAGTTACAGATTTACAGATAACCAATGGAAGGCAGGGAGGCAGAACACAGCCTGCCTGGT  
TCCATCAGCCCTGGGCCAGGCAGCATCTGACTCGGCACCCCTGCAGGCACCATGGCCCAGAGCCGGGTGCTGC  
TGCTCCTGCTGCTGCTGCCACAGCTGCACTGGGACCTGTGCTTGCCGTAGGGCCCCAGGATTGGCGAA  
GTGGCGCCACAGCCTGAGCCCCGAAGAGAACGAATTGCGGGAGGAGGAGGCCGGTGTGACTGAGCCCTGAGG  
AGCCCGGGCTGGCCAGCCGGTCAAGCTGCCCGAGACTGTGCTCTGGCCAGGAGGGCGTGTGACTGTG  
GCGGTATTGACCTGCGTGAAGTCCCGGGGACCTGCTGAGCACCCAACCACCTATCTCTGAGAACAAACCAGC  
TGGAAAAGATCTACCCCTGAGGAGCTCTCCCGCTGCACTGGAGACACTGAACCTGCAAAAACACCGCCTGA  
CTTCCCAGGGCTCCAGAGAAGGCGTTGAGCATCTGACCAACCTCAATTACCTGTACTTGGCCAATAAACAGC  
TGACCTTGGCACCCGCTTCTGCCAAACGCCCTGATCAGTGTGACTTGTGCTGCCAACATATCTACCAAGATCT  
ATGGGCTCACCTTGGCCAAGGCAAACCTTGAGGTCTGTGTACCTGACAAAACAAAGCTGGCAGACGCCGGG  
TGCCGGACAACATGTTCAACGGCTCCAGCAACGTCAGGCTCTCATCTGTCCAGCAACTTCTGCGCACGTGC  
CCAAGCACCTGCCCTGCCGTACAAGCTGCAACCTCAAGAACAAACAGCTGGAGAAGATCCCCCGGGGCT  
TCAGCGAGCTGAGCAGCTGCGAGCTATACTGAGAACAAACTACCTGACTGAGCAGGGCCTGGACAACGAGA  
CCTTCTGGAAGCTCTCAGCCTGGAGTACCTGGATCTGTCCAGCAACAAACCTGTCCTGGGCTCCAGCTGGGCTG  
CGCGCAGCCTGGTGTGCTGCACTTGAGAAGAACGCCATCCGGAGCGTGGACCGGAATGTGCTGACCCCCATCC  
GCAGCCTGGAGTACCTGCTGCTGCACAGCAACCAGCTGCCGGAGCAGGGCATCCACCCACTGGCCTTCCAGGGC  
TCAAGCGGTTGCACACGGTGCACCTGACAACAAACGCGTGGAGCGCGTGCCTGGCTGCCAGTGGCTGCC  
GCACCCCTCATGATCCTGCACAACCAGATCACAGCATTGGCGGAAGACTTGGCACCACCTACTTCTGGAGG  
AGCTCAACCTCACTACAACCGCATCACCGCCACAGGTGACCGCAGCCTCGCAAGCTGCGCTGCTGC  
GCTCGCTGGACCTGTCGGGCAACGGCTGCAACGCTGCCACCTGGGTCCTCGAAATGTCATGTGCTGAAGG  
TCAAGCGCAATGAGCTGGCTGCCCTGGCACAGGAGGGCGTGGCGGGCATGGCTCAGTGTGAGCTGTACCTCA  
CCAGCAACCGACTGCCAGCCGAGCCCTGGGCCCCCTGCTGGTGGACCTCGCCCATCTGAGCTGCTGGACA  
TCGCCGGGAATCAGCTCACAGAGATCCCCGAGGGGCTCCCGAGTCACITGAGTACCTGTCAGAACACA  
AGATTAGTGCCTGGCCGCAATGCTCCGACTCCGACAGCAGCCAACTCAAGGGGATCTTCAGGTTAACAGC  
TGGCTGTGGCTCGTGGTGGACAGTGCCTCCGGAGGCTGAAGGCACCTGCAAGGTCTGGACATTGAAGGCAACT  
TAGAGTTGGTGAACATTCCAAGGACCGTGGCCGCTTGGGAAGGAAAGGAGGAGGAGGAAGAGGAGGAGGAGG  
AGGAAGAGGAAACAAGATAGTGACAAGGTGATGAGATGTGACCTAGGTGATGGACGCCGACTCTTCTGC  
AGCACACGCCGTGCTGAGCCCCCACTCTGCCGTGTCACACAGACACACCCAGCTGCACACATGAGGCA  
TCCCATGACACGGGCTGACACAGTCTCATATCCCCACCCCTCCACGGCGTGTCCCACGGCCAGACACATGC  
ACACACATCACACCCCTCAAACACCCAGCTCAGCCACACACAACTACCCCTCAAACACCACAGTCTGTACAC  
CCCCACTACCGCTGCCACGCCCTCTGAATCATGCAGGGAAAGGTCTGCCCTGGCACACACAGGCACCA  
TTCCTCCCCCTGTCGACATGTGATGCTGATGCAACACACCACACACACATGCACAAGTCATGTGCGAA  
CAGCCCTCAAAGCCTATGCCACAGACAGCTTGGCCAGCCAGAATCAGGCACTAGCAGCTGCCGTGCC  
GTCCATCTGTCGCTCCGTTCCCTGGAGAAGACACAAGGTATCCATGCTGTGGCCAGGTGCCACCCCT  
GGAACTCACAAAGCTGGCTTATTCCCTTCCATGGGACAGGAGCCTCAGGACTGCTGGCCTGGCC  
TGGCCACCCCTGCTCCTCCAGGTGCTGGCAGTCACTCTGTAAGAGTCCCTCCCTGCCACGCCCTGGCAGGACA  
CAGGCACTTTCCAATGGGAAGGCCAGTGGAGGCAGGATGGAGAGGCCCTGGGTGCTGCTGGGCTTGGGG  
CAGGAGTGAAGCAGAGGTGATGGGCTGGCTGAGCCAGGGAGGAAGGACCCAGCTGCACCTAGGAGACACCTT  
GTTCTCAGGCCGTGGGGGAAGTTCGGGTGCCATTATTCTTATTCTTAAGGAAAAAAATGATAAAAT  
CTCAAAGCTGATTTCTTGTATAGAAAAACTAATATAAAAGCATTATCCCTATCCCTGAAAAAA

## **FIGURE 108**

MEGEEAEQPAWFHQWPWRPGASDSAPPAGTMAQSRVLLLLLPPQLHLGPVLAVRAPGFGRS  
GGHSLSPPEENEFAEEEPLVLSPEEPGPAAVSCPDCACSQEGVVDCGGIDLREFPGDLP  
EHTNHLSLQNNQLEKIYPEELSRLHRLETNLQNNRLTSRGLPEKAFLTNLNLYLANNK  
LTLPAPRFLPNALISVDFAANYLTKIYGLTFGQKPNLRSVYLHNNKLADAGLPDNMFNGSSNV  
EVLIILSSNFLRHVPKHLPPALYKLHLKNNKLEKIPPGAFSELSSLRELYLQNNYLTDEGLDN  
ETFWKLSSLEYLDLSSNNLSRVPAGLPRSLVLLHLEKNAIRSVDANVLPIRSLEYLLLHSN  
QLREQGIHPLAFQGLKRLHTVHLYNNALERVPSGLPDRVTLMILHNQITGIGREDFATTYF  
LEELNLSYNRITSPOVHRDAFRKLRLRSLDLSGNRLHTLPPGLPRNVHVLKVKRNEALAALA  
RGALAGMAQLRELYLTSNRLRSRALGPRAWVDLAHLQLLDIAGNQLTEIPEGLPESLEYLYL  
QNNKISAVPANAFDSTPNLKGIIFRFNKLAVGSVVDSAFRRLKHLQVLDIEGNLEFGDISKD  
RGRLGKEKEEEEEEEEEEETR

**Signal sequence:**

amino acids 1-48

**N-glycosylation site.**

amino acids 243-247, 310-314, 328-332, 439-443

**Casein kinase II phosphorylation site.**

amino acids 68-72, 84-88, 246-250, 292-296, 317-321, 591-595

**N-myristoylation site.**

amino acids 19-25, 107-113, 213-219, 217-223, 236-242, 335-341,  
477-483, 498-502, 539-545, 548-554

**Leucine zipper pattern.**

amino acids 116-138, 251-273, 258-280, 322-344, 464-486, 471-493,  
535-557

## **FIGURE 109**

# **FIGURE 110**

MDFLLALVLVSSLYLQAAAEDGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCOPVCQP  
RCKHGE CIGPNKCKCHPGYAGKTCNQDLNECGLKPRPCKHRCMNTYGSYKCYCLNGYMLMPD  
GSCSSALTCSMANCQYGCDVVKGQIRCQCPSPGLHLAPDGRTCVDVDECATGRASCPRFQRC  
VNTFGSYICKCHKGFDLMLYIGGKYQCHDIDECSLGQYQCSSFARCVNRGSYKCKCKEGYQG  
DGLTCVYIPKVMIEPSGPIHPKGNGTILKDTGNNNWIPDVGSTWWPPKTPYIPPIITNRP  
TSKPTTRPTPKPTPIPTPPPPPPLPTELRTPLPPTTPERPTTGLTTIAPAASTPPGGITVDN  
RVQTDPQKPRGDVFSQLVHSCNFDHGLCGWIREKDNDLHWEPIRDPAQQQLTVSAAKAPGG  
KAARLVLPLGRLMHSGDLCLSFRHKVTGLHSGLQVFVRKHGAHGAALWGRNGGHGWQTOI  
TLRGADIKSESQR

**Signal sequence:**

amino acids 1-17

**N-glycosylation site.**

amino acids 273-277

**Casein kinase II phosphorylation site.**

amino acids 166-170, 345-349

**Tyrosine kinase phosphorylation site.**

amino acids 199-206

**N-myristoylation site.**

amino acids 109-115, 125-131, 147-153, 191-197, 221-227, 236-242,  
421-427, 433-439, 462-468, 476-482

**Aspartic acid and asparagine hydroxylation site.**

amino acids 104-116, 186-198, 231-243

**Cell attachment sequence.**

amino acids 382-385

**EGF-like domain cysteine pattern signature.**

amino acids 75-87

## **FIGURE 111**

CTTCTTTGAAAAGGATTATCACCTGATCAGGTTCTCTGCATTGCCCTTAGATTGTGA  
**AATGTGGCTCAAGGTCTTCACAAC**TTCCCTTGCACAGGGTCTGCTCGGGGCTGA  
AGGTGACAGTGCCATCACACACTGTCCATGGCGTCAGAGGTCAAGGCCCTACCTACCCGTC  
CACTATGGCTTCCACACTCCAGCATCAGACATCCAGATCATATGGCTATTGAGAGACCCA  
ACAATGCCAAATACTTACTGGGCTCTGTGAATAAGTCTGTGGTCTGACTTGAATACC  
AACACAAGTTCAACCATGATGCCACCCAAATGCATCTGCTTATCAACCCACTGCAGTTCCCT  
GATGAAGGCAATTACATCGTAAGGTCAACATTCAAGGAAATGGAACACTATCTGCCAGTCA  
GAAGATAACAAGTCACGGTTGATGATCCTGTACAAAGCCAGTGGTGCAGATTCATCCTCCCT  
CTGGGGCTGTGGAGTATGTGGGAACATGACCCCTGACATGCCATGTGGAAGGGGGCACTCGG  
CTAGCTTACCAATGGCTAAAAAATGGGAGACCTGTCCACACCAGCTCCACCTACTCCTTTTC  
TCCCCAAAACAATACCCCTCATATTGCTCCAGTAACCAAGGAAGACATTGGAATTACAGCT  
GCCTGGTGAGGAACCCCTGTCAGTGAATGGAAAGTGAATCATATTGCCATCATATTAT  
GGACCTTATGGACTTCAAGTGAATTCTGATAAAGGGCTAAAAGTAGGGGAAGTGTACTGT  
TGACCTTGGAGAGGCCATCCTATTGATTGTTCTGCTGATTCTCATCCCCCAACACCTACT  
CCTGGATTAGGAGGACTGACAATACTACATATCATTAAGCATGGGCCTCGCTAGAAGTT  
GCATCTGAGAAAGTAGCCCAGAAGACAATGGACTATGTGTGCTGTGCTTACAACACATAAC  
CGGCAGGCAAGATGAAACTCATTCACAGTTATCATCACTCCGTAGGACTGGAGAAGCTTG  
CACAGAAAGGAAAATCATTGTCACCTTAGCAAGTATACTGGAATATCACTATTGATT  
ATATCCATGTGTCTTCTCTTCTATGGAAAAAATATCAACCTACAAAGTTATAAAACAGAA  
ACTAGAAGGCAGGCCAGAACAGAACATCAGGAAAGCTCAAACATTTCAGGCCATGAAGATG  
CTCTGGATGACTTCGGAATATATGAATTGTTGCTTCCAGATGTTCTGGTGTCCAGG  
ATTCCAAGCAGGTCTGTTCCAGCCTCTGATTGTATGGGCAAGATTGCACAGTACAGT  
GTATGAAGTTATTCAAGCACATCCCTGCCAGCAGCAAGACCATTCAAGTTGAACTTCATGG  
GCTAAACAGTACATTGAGTGAAAATTCTGAAGAACATTAAAGGAAAACAGTGGAAAAGT  
ATATTAAATCTGGAATCACTGAAGAACCAGGACCAACACCTCTACTCATTATTCTTACA  
TGCAGAACAGGATTATGCAAATTGAACTGCAGGTTTCAGCATATAACAAATGTCTT  
GTGCAACAGAAAACATGTTGGGAAATATTCCCTCAGTGGAGAGTCGTTCTCATGCTGACGG  
GGAGAACGAAAGTGACAGGGTTCTCATAAGTTGTATGAAATATCTACAAACCTCA  
ATTAGTTCTACTCTACACTTCACTATCATCAACACTGAGACTATCCTGCTCACCTACAAA  
TGTGGAAACTTACATTGTTCGATTTCAGCAGACTTGTGTTATTAAATTGTTATTAGTG  
TTAAGAATGCTAAATTATGTTCAATTATTCCAAATTCTATCTTGTATTTGACAA  
CAAAGTAATAAGGATGGTTGTACAAAACAAACTATGCCCTCTTTTTCAATCACC  
AGTAGTATTGAGAAGACTGTGAACACTTAAGGAAATGACTATTAAAGTCTTATTGTTA  
TTTTTTCAAGGAAAGATGGATTCAAATAATTCTGTTTGCTTAAAAAAA

## **FIGURE 112**

MWLKVFTTFLSFATGACSGLKVTVPSPHTVHGVRGQALYLPVHYGFHTPASDIQIIWLFERPH  
TMPKYLLGSVNKSVPDLEYQHKFTMMPPNASLLINPLQFPDEGNYIVKVNIQGNGLTLSASQ  
KIQVTVDPPVTKPVVQIHPPSGAVEYVGNMTLTCHEGGTRLAYQWLKNGRPVHTSSTYSFS  
PQNNTLHIAPVTKEIDIGNYSCLVRNPVSEMESDIIMPIIYYGPYGLQVNNSDKGLKVGEVFTV  
DLGEAILFDCSADSHPPNTYSWIRTDNTTYIIKHGPRLEVASEKVAQKTMDYVCCAYNNIT  
GRQDETHFTVIITSVGLEKLAQKGKSLSPLASITGISLFLIISMCLLFLWKKYQPYKVIKQK  
LEGRPETEYRKAQTFSGHEDALDDFGIYEFPDVSGVSRIPSRSVPASDCVSGQDLHSTV  
YEVIOQHIPAQQQDHPE

**Signal sequence:**

amino acids 1-18

**Transmembrane domain:**

amino acids 341-359

**N-glycosylation site.**

amino acids 73-77, 92-96, 117-121, 153-157, 189-193, 204-208,  
276-280, 308-312

**Casein kinase II phosphorylation site.**

amino acids 129-133, 198-202, 214-218, 388-392, 426-430, 433-437

**Tyrosine kinase phosphorylation site.**

amino acids 272-280

**N-myristoylation site.**

amino acids 15-21, 19-25, 118-124, 163-167, 203-209, 231-237,  
239-245

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18

## **FIGURE 113**

GCAAGCGGC~~GAAATGGCGCCCTCCGGGAGTCTTCAGTTCCCTGGCAGTCCTGGTGTGTT~~  
GCTTG~~GGGTGCTCCCTGGACGCACGGCGGCCGGAGCAACGTTCCGTCATCACGGACGAGA~~  
ACTGGAGAGAA~~CTGCTGGAAGGAGACTGGATGATAGAATTATGCCCCGTTGCCCCTGCT~~  
TGTCAA~~AAATCTCAACCAGGAATGGGAAAGTTGCTGAATGGGAGAAGATCTTGAGGTTAA~~  
TATTG~~CAGAAGTAGATGTACAGAGCAGCCAGGACTGAGTGGACGGTTATCATAACTGCTC~~  
TTC~~CTACTATTATCATTGTAAGATGGTGAATTAGGCCTATCAGGGCCAAGGACTAAG~~  
AAGGACT~~TCAAACTTATAAGTGATAAAGAGTGGAAAGAGTATTGAGCCGTTCATCATG~~  
GTTTGGT~~CCAGGTTCTGTTCTGATGAGTAGTATGTCAGCACTCTTCAGCTATCTATGTGGA~~  
TCAGGAC~~GTCATAACTACTTATTGAAGACCTTGGATTGCCAGTGTGGGATCATATACT~~  
GTTTG~~CCTTAGCAACTCTGTTCCGGACTGTTATTAGGACTCTGTATGATATTGTG~~  
AGATTG~~CCTTGTCCCTCAAAAAGGCCAGACCCACAGCCATACCCATACCCCTCAAAAAAAT~~  
TATTATC~~AGAATCTGCACAACCTTGAAAAAGTGGAGGAGGAACAAGAGGCCGATGAAGAA~~  
GATG~~TTCAAGAAGAAGCTGAAAGTAAAGAAGGAACAAACAAAGACTTCCACAGAATGC~~  
CAT~~AAGACAACGCTCTGGGCCATCATTGGCACAGATAAACCTAGTTAAATT~~  
TTATCT~~TAATATTATGATTTGATAAAACAGAAGATTGATCATTGTTGGTTGAAGTG~~  
AACTGT~~GACTTTTGAAATATTGCAAGGTTCACTGATGTTGATTAAGAGTCTA~~  
CATT~~CAGAACATAAAAGCACTAGGTATACAAGTTGAAATATGATTAAGCACAGTATGATG~~  
GTT~~AAATAGTTCTTAATTGAAAAACGTGCCAGCAATAAGATTATGTATATTGT~~  
TTAATA~~AAACCTATTCAAGTCTGAGTTGAAAATTACATTCCCAAGTATTGATT~~  
TGAGG~~TATTAGAAGATTATTAGAGAAAATATTCTCATTTGATATAATTCTCTG~~  
TT~~TCAGTGTGAAAAAGAAGATATTCCCATAATGGGAAGTTGCCATTGTCTCAAG~~  
AAATGT~~GTTTCAGTGCACATTCTGGTCTTTAGAGGTATATTCCAAATTCTCTG~~  
ATTTT~~AGGTATGCAACTAAACACTACCTACATTAAATTACAGTTCTACACA~~  
TGG~~TAATACAGGATATGCTACTGATTAGGAAGTTTAAGTTCATGGTATTCTTGATTC~~  
CAAC~~AAAGTTGATTCTCTGTATTCTTACTTACTATGGGTACATTTTATT~~  
CAA~~ATTGGATGATAATTCTGGAAACATTTTATGTTAGTAAACAGTATTGTTGTT~~  
GTT~~CAAACGTTGAAAGTTACTGAGAGATCCATCAAATTGAACAATCTGTTGTAATT~~  
TTGCC~~ACTTTTCAGATTTACATCATTCTGCTGAACCTCAACTGAAATTGTTTTT~~  
TTCT~~TTGGATGTAAGGTGAACATTCTGATTGTTCTGATGTGAAAAAGCCTGGTA~~  
TTT~~TACATTGAAAATTCAAAGAAGCTTAATATAAAAGTTGCATTCTACTCAGGAAAAG~~  
CAT~~CTTCTGTATATGCTTAAATGTATTGTCCTCATATACAGAAAGTTCTTAATTGAT~~  
TT~~TACAGTCTGTAATGCTGATGTTAAAATAACATTATATTGTTAAAGACAA~~  
ACT~~TCAATTATCCTGTTCTGACTGGTAATATTGTTGAGGATTCACAGGTAAA~~  
GTC~~CAGTAGGATGGAACATTAGTGTATTGACTCCTTAAAGAGCTAGAATACATAGTTT~~  
CAC~~CTTAAAGAAGGGGAAATCATAAATACAATGAATCAACTGACCATTACGTAGTAC~~  
AATT~~TCTGTAATGTCCTCTTCTAGGCTCTGTTGCTGTGAATCCATTAGATTACAG~~  
TAT~~CGTAATATACAAGTTCTTAAAGCCCTCCTTCTAGAATTAAAATATTGTACCA~~  
AAAG~~AGTTGGATGTAACTTGTGATGCCTAGAAAAATATCCTAACGACAAAATAAC~~  
TT~~CTAACCACTTCATTAAGCTGAAAAAAAAAAAAAA~~

## **FIGURE 114**

MAPSGSLAVPLAVLVLLLWGAPWTHGRRSNVRVITDENWRELLEGDWMI  
EFYAPWCPACQNL  
QPEWESFAEWGEDLEVNIAKVDVTEQPGLSGRFIITALPTIYHCKDGEFRRYQGPRTKKDFI  
NFISDKEWKSIEPVSSWFGPGSVLMSSMSALFQLSMWIRTCHNYFIEDLGLPVWGSYTVFAL  
ATLFSGLLLGLCMIFVADCLCPSKRRPQPYPYPSKKLLSESAQPLKKVEEEQEADEEDVSE  
EEAESKEGTNKDFPQNAIRQRSLGPSLATDKS

**Signal sequence:**

amino acids 1-26

**Transmembrane domain:**

amino acids 182-201

**Casein kinase II phosphorylation site.**

amino acids 68-72, 119-123, 128-132, 247-251, 257-261

**Tyrosine kinase phosphorylation site.**

amino acids 107-115

**N-myristoylation site.**

amino acids 20-26, 192-198

**Amidation site.**

amino acids 25-29

## **FIGURE 115**

GCGAGTGTCCAGCTGGAGACCCGTGATAATTGTTAACTAATTCAACAAACGGGACCCTT  
CTGTGTGCCAGAAACCGCAAGCAGTGTGCTAACCCAGTGGGACAGGCAGGATTGGAAGAGCAGGG  
AAGTCCTGGCCCAGAGCAGTGTGACACTTCCCTCTGTGACCTGAAACTCTGGGTGTCTGC  
ATTGCTGATGGCCTGGTTGGTGTCTGAGCTGTGTCAGGGCAATTCTCACCTCTATTG  
GGCACATGACTGACCTGATTATGCAGAGAAAGAGCTGGTGAGTCTGTGAAAGAGTACATC  
CTTGTGGAGGAAGCCAAGCTTCCAAGATTAAGAGCTGGCCAACAAAATGGAAGCCTTGAC  
TAGCAAGTCAGCTGCTGATGCTGAGGGCTACCTGGCTCACCTGTGAATGCCCTACAAACTGG  
TGAAGCGGCTAACACACAGACTGGCCTGCGCTGGAGGACCTTGTCTGCAGGACTCAGCTGCA  
GGTTTTATGCCAACCTCTGTGCGAGCGGAGTTCTCCCCACTGATGAGGACGAGATAGG  
AGCTGCCAAAGCCCTGATGAGACTTCAGGACACATACAGGCTGGACCCAGGCACAATTCCA  
GAGGGGAACCTCCAGGAACCAAGTACCAAGGCAATGCTGAGTGTGGATGACTGCTTGGATG  
GGCCGCTCGGCCTACAATGAAGGGACTATTATCATACGGTGTGGATGGAGCAGGTGCT  
AAAGCAGCTTGATGCCGGGAGGAGGCCACCAACCAAGTCACAGGTGCTGGACTACCTCA  
GCTATGCTGTCTTCCAGTTGGGTGATCTGCACCGTGCCTGGAGGCTCACCCGCCCTGCTC  
TCCCTGACCAAGCCACGAGCTGGAGGAATCTCGGTACTTGAGCAGTTATTGGA  
GGAAGAGAGAGAAAAACGTTAACAAATCAGACAGAAGCTGAGCTAGCAACCCCAGAAGGCA  
TCTATGAGAGGCCTGTGGACTACCTGCCTGAGAGGGATGTTACGAGAGCCTCTGCGTGGG  
GAGGGTGTCAAACGTACACCCGTAGACAGAAGAGGCTTCTGTAGGTACCAACATGGCAA  
CAGGGCCCCACAGCTGCTATTGCCCTTCAAAGAGGAGGAGCTGGACAGCCGCACA  
TCGTCAAGGTACTACGATGTCATGTGATGAGGAAATCGAGAGGATCAAGGAGATCGAAAAA  
CCTAAACTTGCACGAGCCACCGTCTGTGATCCCAAGACAGGAGTCTCAGTCGCCAGCTA  
CCGGGTTCCAAAGCTCTGGCTAGAGGAAGATGATGACCCCTGTTGTGGCCGAGTAAATC  
GTCGGATGCAGCATATCACAGGGTTAACAGTAAGACTGCAGAATTGTTACAGGTTGCAAAT  
TATGGAGTGGGAGGACAGTATGAACCGCACTCGACTTCTCTAGGCGACCTTTGACAGCGG  
CCTAAAACAGAGGGAAATAGGTTAGCGACGTTCTTAACACATGAGTGTAGAACAGCTG  
GTGGTGCACCGTCTCCCTGATCTGGGGCTGCAATTGGCTAAGAAGGGTACAGCTGTG  
TTCTGGTACAACCTCTGGAGCGGGGAAGGTGACTACCGAACAGACATGCTGCCTGCC  
TGTGCTTGTGGCTGCAAGTGGGTCTCCAATAAGTGGTCCATGAACGAGGACAGGAGTTCT  
TGAGACCTTGTGGATCAACAGAAGTTGACTTGACATCCTTCTGCTCTCCCTCTGGTC  
CTTCAGCCCATGTCAACGTGACAGACACCTTGTATGTTCTTGTATGTTCTATCAGGCT  
GATTTTGAGGAAATGAATGTTGTCTGGAGCAGAGGGAGACCATACTAGGGCGACTCCTGT  
GTGACTGAAGTCCCAGCCCTTCCATTCAAGCCTGTGCCATCCCTGGCCCAAGGCTAGGATCA  
AAAGTGGCTGAGCAGAGTTAGCTGTCTAGCGCTAGCAAGGTGCTTGTACCTCAGGTGTT  
TTAGGTGTGAGATGTTCAAGTGAACCAAGTTCTGATACCTGTTACATGTTGTTTAT  
GGCATTCTATCTATTGTGGCTTACCAAAAAAATGTCCCTACCAGAAAAAA

## **FIGURE 116**

MKLWVSALLMAWFGVLSCVQAEFFTSIGHMTDLIYAEKELVQSLKEYILVEEAKLSKIKSWA  
NKMEALTSKSAADAEGYLAHPVNAYKLVKRLNTDWPALEDLVLQDSAGFIANLSVQRQFFP  
TDEDEIGAAKALMRLQDTYRLDPGTISRGELPGTKYQAMLSVDDCFGMGRSAYNEGDYYHTV  
LWMEQVLKQLDAGEEATTTKSQVLDYLSYAVFQLGDLHRAELTRRLLSLDPSHERAGGNLR  
YFEQLLEEEEREKTLTNQTEAELATPEGIYERPVDYLPERDVYESLCRGEGVKLTPRQKRLF  
CRYHHGNRAPQLLIAPFKEEDEWDSPHIVRYYDVMSDEEIERIKEIAKPKLARATVRDPKTG  
VLTVASYRVSKSSWLEEDDPVVARVNRRMQHITGLTVKTAELLQVANYGVGGQYEPHFDFSGEVDYR  
RRPFDDSGLKTEGNRLATFLNYMSDVEAGGATVFPDLGAIWPKKGTAVFWYNLLRSGEGDYR  
TRHAACPVLVGCKWVSNKFHERGQEFLRPCGSTEVD

**Signal sequence:**

amino acids 1-17

**N-glycosylation site.**

amino acids 115-119, 264-268

**Glycosaminoglycan attachment site.**

amino acids 490-494

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 477-481

**Casein kinase II phosphorylation site.**

amino acids 43-47, 72-76, 125-129, 151-155, 165-169, 266-270,  
346-350, 365-369, 385-389, 457-461, 530-534

**Tyrosine kinase phosphorylation site.**

amino acids 71-80, 489-496

**N-myristoylation site.**

amino acids 14-20, 131-137, 171-177, 446-452

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 8-19

**Leucine zipper pattern.**

amino acids 213-235

## **FIGURE 117**

GCAGTATTGAGTTTACTTCCTCTTTAGTGAAGACAGACCATAATCCAGTGTGAGTGAAATTGATTGT  
TTCATTTATTACCGTTTGGCTGGGGTTAGTCCGACACCTTCACAGTGAAGAGCAGGCCAGAAGGAGTTGTGA  
AGACAGGACAATCTTCTGGGGATGCTGGCTTGAAGCCAGCAGGGCTTGCTCTGTCTTGGCCTCATGACCC  
CAGGTTCTCTGGTTAAACTGAAAGCCTACTACTGGCTGGCCATCAATCATTGATCCTTGAGGCTGTGCC  
CCTGGGGCACCCACCTGGCAGGGCTACCAACCATGCAGTGCAGCTCCCTGTTGGCTCTGCTGCCAGCGCTTC  
CCCTCATCTTAGGGCTCTCTGGGGTGCAGCCTGAGCCTCTGCGGGTTCTGGATCCAGGGGAGGGAGAAG  
ATCCCTGTGTCGAGGCTGAGGGAGCCACAGAACATCCAGATTGAGAGCTGGCTAGACCAAAGTG  
ATGAAGACTTCAAACCCGGATTGTCCTACTACAGGGACCCAAACAAGCCTACAAGAAGGTGCTCAGGACTC  
GGTACATCCAGACAGAGCTGGCTCCTGGCTGAGCGGTTGCTGCTGACCTCCGAGCTACACTGTCCA  
CTTGGCCGTGGCTGTGAACCGTACGGTGGCCATCACTCCCTCGGTTACTCTACTTCACGGCAGGGGG  
CCCAGGCTCCAGCAGGGATGCGAGTGGTGTCTATGGGATGAGCGGGCCCTGGCTATGTCAGAGACCCCTGC  
GCCACCTTCACACACACTTGGGCCGACTACGACTGGTCTTACATCATGCGAGATGACACATATGTCAGGCC  
CCGGCCTGGCAGCCCTGCTGGCCACCTCAGCATCAACCAAGACCTGACTTACGGCCGGAGAGGATTGATTG  
GCGCAGCGAGCAGGCCGGTACTGTCATGGGGCTTGCTACCTGTTGTCACGGAGTCTCCTGCTCGCTGC  
GGCACATCTGGATGGCTGCCGAGGAGACATTCTAGTGGCCCTGACGAGTGGCTGGACGCTGCTCATTG  
ACTCTCTGGCGTCTGGCTGTCACAGCACCAGGGCAGCAGTATGCTCATTTGAACTGGCCAAAATAGGG  
ACCCCTGAGAAGGAAGGGAGCTGGCTTCCCTGAGTGCCITGCCGTGACCCCTGCTCCGAAGGTACCCCTATGT  
ACCGGCTCCACAAACGCTTCAGCGCTCTGGAGTTGGAGGGCTTAAGTGAATAGAACAACTGCAGGCTCAGA  
TCCGGAACCTGACCGTGTGACCCCCGAAGGGAGGCAGGGCTGAGCTGGCCGGTTGGCTCCCTGCTCATTCA  
CACACACACTCTGCTTTGAGGTGCTGGCTGGACTACTTCACAGACGACACACCTCTCCTGTGCAAGATGGGG  
CTCCAAGTGCCACTACAGGGGCTAGCAGGGCGACGTGGGTGATGCCGTGGAGACTGCCCTGGAGCAGCTCA  
ATCGCGCTATCAGCCCCCTGCCCTGCGCTTCAAGCAGCAGCTCAACGGCTATCGCGCTTCGACCCAGCAC  
GGGCATGGAGTACACCCCTGGACCTGCTGTTGAAATGTGTGACACAGCGTGGCACCGGGGGCCCTGGCTCGA  
GGGTCAGCCTGCTGCCACTGAGCCGGGTGAAATCCTACCTATGCCCTATGTCACTGAGGCCACCCAGTGC  
AGCTGGTGTGCCACTCTGGTGGCTGAAGCTGCTGCAAGCCGGCTTCCCTGAGGCGTTGCAAGCCATGTCC  
TGGAGCCACGAGAACATGCTACCCCTGTTGCTACGGGCCACGAGAACGGTGGCCGTGGAGCTCCAG  
ACCCATTCTGGGGTGAAGGCTGCAGCAGCGAGTTAGAGCGACGGTACCCCTGGGACGAGGCTGGCTGGCTCG  
CTGTGCGAGCAGGCCCTTCCAGGTGCGACTCATGGACGTGGTCTGAAGAAGCACCCTGTTGACACTCTCT  
TCTTCTTACCCCGTGGCAAGGCCCTGGGGCGAAGTCTCAACCGCTGTCGATGAATGCCATCTGGCT  
GGCAGGCCCTTCCAGTCATTTCCAGGAGTCAATCTGCCCTGTCACCACAGAGATCACCCCCAGGGCCCC  
CGGGGGCTGCCCTGACCCCCCTCCCTGGCTGACCCCTCCGGGGGCTCTATAGGGGGAGATTG  
ACCGGCAGGCTCTGCCGGAGGCTGCTTACAACGCTGACTACCTGGCGGCCAGGCCGGCTGGCAGGTGAAC  
TGGCAGGCCAGGAAGAGGAGGAAGCCCTGGAGGGGCTGGAGGGTATGGATGTTTCTCCGGTTCTCAGGGCTCC  
ACCTCTTCGGCCGTAGAGCCAGGGCTGGTGAGAACAGTTCTCCCTGCGAGACTGCAGCCCACGGCTCAGTGAAG  
AACTCTACCAACCGCTGCCCTCAGCAACCTGGAGGGCTAGGGGGCCGTGCCAGCTGGCTATGGCTCTTTG  
AGCAGGAGCAGGCCAATAGCACTTAGCCCGCCTGGGGCCCTAACCTCATTACCTTCTGTCTGCCAGCC  
CCAGGAAGGGCAAGGCAAGATGGTGGACAGATAGAGAATTGTTGCTGATTTTAAATATGAAAATGTTATTAA  
ACATGTCTCTGCC

## **FIGURE 118**

MRLSSLLALLRPALPLILGLSLGCSLSLLRVSWIQGEGEDPCVEAVGERGGPQNPDSRARLD  
QSDEDFKPRIVPYYRDPNPKVLRTRYIQTTELGSERLLVAVLTSRATLSTLAVAVNRTV  
AHHFPRLLYFTGQRGARAPAGMQVVSHGDERPAWLMSETLRHLHTHFGADYDWFFIMQDDTY  
VQAPRLAALAGHLSINQDLYLGRAEEFIGAGEQARYCHGGFGYLLSRSLLLRLRPHLDGCRG  
DILSARPDEWLGRCLIDS LGVGCVSQHQGQQYRSFELAKNRDPEKEGSSAFLSAFAVHPVSE  
GTLMYRLHKRFSALELERAYSEIEQLQAQIRNLTVLTPEGEAGLSPVGLPAPFTPNSRFEV  
LGWDYFTEQHTFSCADGAPKCPLQGASRADVGALETALEQLNRRYQPRLRFQKQRLLNGYR  
RFDPARGMEYTLDLLCEVTQRGHRRRALARRVSLLRPLSRVEILPMPYVTEATRVQLVLPLL  
VAEAAAAPAFLEFAANVLEPREHALLTLLVYGPREGGRGAPDPFLGVKAAAELERRYPG  
TRLAWLAVRAEAPSQVRLMDVVSKKHPVDTLFFLTTVWTRPGPEVLRNRCRMAISGWQAFFP  
VHFQEFPALSPQRSPPGPPGAGPDPPSPPGADPSRGAPIGGRFDRQASAEGCFYNADYLAA  
RARLAGELAGQEEEALEGLEVMDFVFLRFSGLHLFRAVEPGLVQKFSLRDCSPRLSEELYHR  
CRLSNLEGLGGRQLAMALFEQEQQANST

**Signal sequence:**

amino acids 1-15

**Transmembrane domain:**

amino acids 489-507

**N-glycosylation site.**

amino acids 121-125, 342-346

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 319-323, 464-468

**Casein kinase II phosphorylation site.**

amino acids 64-68, 150-154, 322-326, 331-337, 368-372, 385-389,  
399-403, 409-413, 473-477, 729-733, 748-752

**Tyrosine kinase phosphorylation site.**

amino acids 736-743

**N-myristoylation site.**

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,  
558-564, 651-657, 657-663, 672-678

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 14-25

**Cell attachment sequence.**

amino acids 247-250

## **FIGURE 119**

CGGAGTGGTGCACGTGAGAGGAAACCGTGCACGGCTGCCTTCCTGTCCCCAAGCC  
GTTCTAGACGCCGGAAAAATGCTTCTGAAAGCAGCTCCTTTGAAGGGTGTATGCTTGG  
AACATTTCTGTGCTTGATCACTATGCTAGGACACATTAGGATTGGCATGGAAATAGAA  
TGCACCACCATGAGCATCATCACCTACAAGCTCTAACAAAGAAGATATCTGAAAATTCA  
GAGGATGAGCGCATGGAGCTCAGTAAGAGCTTCAGTATACTGTATTATCCTGTAAAACC  
CAAAGATGTGAGTCTTGGGCTGCAGTAAAGGAGACTGGACAAACACTGTGACAAAGCAG  
AGTTCTCAGTTCTGAAAATGTTAAAGTGTGAGTCATTAATATGGACACAAATGACATG  
TGGTTAATGATGAGAAAAGCTTACAAATACGCCCTTGATAAGTATAGAGACCAATACAAC  
GTTCTCCTGCACGCCCACTACGTTGCTATCATTGAAAACCTAAAGTATTTTGTAA  
AAAAGGATCCATCACAGCCTTCTATCTAGGCCACACTATAAAATCTGGAGACCTTGAATAT  
GTGGGTATGGAAGGAGGAATTGTCTTAAGTGTAGAATCAATGAAAAGACTTAACAGCCTCT  
CAATATCCCAGAAAAGTGTCTGAACAGGGAGGGATGATTGGAAGATATCTGAAGATAAAC  
AGCTAGCAGTTGCCTGAAATATGCTGGAGTATTGCAAGAAAATGCAGAAGATGCTGATGGA  
AAAGATGTATTTAATACCAAATCTGTTGGCTTCTATTAAAGAGGCAATGACTTACACCC  
CAACCAGGTAGTAGAAGGCTGTTAGATATGGCTGTTACTTTAATGGACTGACTCCAA  
ATCAGATGCATGTGATGTATGGGTATACCGCCTTAGGGCATTGGCATATTTCAAT  
GATGCATTGGTTCTTACCTCAAATGGTCTGACAATGACTGAGAAGTGGTAGAAAAGCG  
TGAATATGATCTTGTATAGGACGTGTGTCATTATTGTAGTAGTAACATACATCCAA  
TACAGCTGTATGTTCTTTCTTAATTTGGTGGCACTGGTATAACCACACATTAAAG  
TCAGTAGTACATTTAAATGAGGGTGGTTTTCTTAAAACACATGAACATTGAAATG  
TGTTGGAAAGAAGTGTGTTAAGAATAATAATTGCAAATAACTATTAAATAATTAT  
GTGATAAATTCTAAATTATGAACATTAGAAATCTGTGGGGCACATATTTGCTGATTGGTT  
AAAAAAATTAAACAGGTCTTAGCGTTCTAAGATATGCAAATGATATCTCTAGTTGTGAATT  
TGTGATTAAAGTAAAACCTTGTGTTCCCTTACTCTAATACTGATTATGTTCT  
AAGCCTCCCCAAGTCCAATGGATTGCCTCTCAAATGTACAACTAAGCAACTAAAGAAA  
ATTAAAGTGAAGTGTAAAAAT

## **FIGURE 120**

MLSESSSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHHEHHHLQAPNKEDILKISEDERME  
LSKSFRVYCIILVKPKDVSLWAAVKETWTKHCDKAEFFSSENVKFESINMDTNMDWLMMRK  
AYKYAFDKYRDQYNWFFLARPTTFAIENLKYFLLKKDPSQPFYLGHТИKSGDLEYVGMEGG  
IVLSVESMKRLNSLLNIPEKCPEQGGMIWKISEDKQLAVCLKYAGVFAENAEDADGKDVFNT  
KSVGLSIKEAMTYHPNQVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFGHIFNDALVFL  
PPNGSDND

**Signal sequence:**

amino acids 1-33

**N-glycosylation site.**

amino acids 121-125, 342-346

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 319-323, 464-468

**Casein kinase II phosphorylation site.**

amino acids 64-132, 150-154, 322-326, 331-335, 368-372, 385-389,  
399-403, 409-413, 473-477, 729-733, 748-752

**Tyrosine kinase phosphorylation site.**

amino acids 736-743

**N-myristoylation site.**

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,  
558-564, 651-657, 657-663, 672-672

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 14-25

**Cell attachment sequence.**

amino acids 247-250

## **FIGURE 121**

## **FIGURE 122**

MNSSKSSETQCTERGCSSQMFLWTVAGIPILFLSACFITRCVVTFRIFQTCDEKKFQLPEN  
FTELCYNYGSGSVKNCCPLNWEYFQSSCYFFSTDTISWALSLKNCSAMGAHLVVINSQEEQ  
EFLSYKKPKMREFFIGLSDQVVEGQWQWVDGTPLTKSLSFWDVGEPPNNIATLEDCATMRDSS  
NPRQNWNDVTCFLNYFRICEMVGINPLNKGS

**Signal sequence:**

amino acids 1-42

**N-glycosylation site.**

amino acids 2-6, 62-66, 107-111

**Casein kinase II phosphorylation site.**

amino acids 51-55, 120-124, 163-167, 175-179, 181-185

**N-myristoylation site.**

amino acids 15-21, 74-80, 155-161

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 27-38

## **FIGURE 123**

GGGACTACAAGCCGCCCGCTGCCGCTGGCCCCCTCAGCAACCTCGACATGGCGCTGAGGCGGCCACCGCGAC  
TCCGGCTCGCGCTCGCTGACTTCTTCCTGCTGCTGCTTTCAAGGGCTGCTGATAAGGGCTGTAAATC  
TCAAATCCAGCAATCGAACCCCAGTGGTACAGGAATTGAAAGTGTGAACTGTCTGCATCATTACGGATTGCG  
AGACAAGTGACCCAGGATCGAGTGGAAAGAAAATTCAAGATGAACAAACCACATATGTGTTTGACAACAAAA  
TTCAGGGAGACTTGGCGGGTCTGCAAGAAATACTGGGAAGACATCCCTGAAGATCTGAATGTGACACGGAGAG  
ACTCAGCCCTTATCGCTGTGAGGTGCTGAAATGACCGAAGGAATTGATGAGATTGTGATCGAGTTAA  
CTGTGCAAGTGAAGCCAGTGACCCCTGCTGTAGAGTGCCGAAGGCTGTACCACTAGTAGGCAAGATGGCAACACTGC  
ACTGCCAGGAGAGTGAGGGCACCCCCGGCCTCACTACAGCTGGTATCGCAATGATGTACCAACTGCCACGGATT  
CCAGAGCCAATCCCAGATTTCGAATTCTCTTCACTTAAACTCTGAAACAGGCACTTGTGTTCACTGCTG  
TTCAACAGGACGACTCTGGGAGACTACTGCAATTGCGGAATTATTGGGGGGTCTGGTGTCTGTACTGCCCTGA  
AGATGGAAGTCTATGACCTGAACATTGGCGGAATTATTGGGGGGTCTGGTGTCTGTACTGCCCTGA  
TCACGGTGGGATCTGCTGTGCAACAGCTGGTACTTCATCAACAATAACAGGATGGAGAAAGTTACAAGA  
ACCCAGGGAAACCAAGATGGAGTTAACATACCCGACTGACGAGGAGGGCACTTCAGACACAAGTCATCGTTG  
TGATCTGAGACCCCGGGTGTGGCTGAGAGCGCACAGAGCGCACGTGCACATACCTCTGCTAGAAAACCTGTCAA  
GGCAGCGAGAGCTGATGCACTCGGACAGAGCTAGACACTCATTCAGAAAGCTTTCTGTTTGGCAAAGTTGACCA  
CTACTCTTACTCTAACAGCCACATGAATAGAAGAATTTCCTCAAGATGGACCCGGTAAATAACCAACAA  
GGAAGCGAAACTGGGTGCGTTACTGAGTTGGGTTCTTAATCTGTTCTGGCCTGATTCCGCATGAGTATTAGG  
GTGATCTAAAGAGTTGCTCACTGAAACGCCGTGCTGGGGCTGTGAAGCCAGCATGTTCAACCCTGGTGT  
CAGCAGCCACGACAGCACCATGTGAGATGGCGAGGTGGCTGGACAGCACCAGCAGCGCATCCGGGGAAACCCA  
GAAAAGGCTTCTTACACAGCAGCCTACTTCATCGGCCACAGACACCACCGCAGTTCTTAAAGGCTCTG  
TGATCGGTGTTGCACTGTCATTGTGGAGAAGCTTTGGATCAGCATTTGTAAGAACACAAAATCAGGAAG  
GTAATTGGTGTGGAAGAGGGATCTGGCTGAGGAACCTGCTTGTCAAACAGGGTGTCAAGGATTAAGGAAA  
ACCTTCGTCTTAGGCTAACTGAAATGGTACTGAAATATGCTTTCTATGGGTCTGTTATTAAACCAAAATT  
TACATCTAAATTGGTCAAGGATGTATTGATTATTGAAAGAAATTCTATTAAACTGTAATATATTGT  
CATACAATGTTAAATAACCTATTGTTAAAAAGTTCAACTTAAGGTTAGAAGTCCAAGCTACTAGTGTAAAT  
TGGAAAATATCAATAATTAAAGATTTTACCAAGGAATCCTCTCATGGAAGTTACTGTGATGTTCTTTCT  
CACACAAGTTTAGCCTTTTCACAAGGAACCTACACTGTCTACACATCAGACCATAGTTGCTTAGGAAACCTT  
TAAAATTCAGTTAACGAAATGTTGAAATCAGTTGCTCTTCAAAAGAAACCTCTCAGGTTAGCTTGAAC  
GCCTCTCCTGAGATGACTAGGAACAGTCTGTACCCAGAGGCCACCCAGAAGGCCCTCAGATGTACACACAGATG  
CCAGTCAGCTCTGGGGTGCAGGCCAGGCCCCCCCTCTAGCTCAGTTGCTCTGCTCTGCCAGGAGGCCCT  
GCCATCCTGGGGCTGGCAGTGGCTGTGCTCCAGTGGCTTACTCACGTGGCCCTTGCTCATCCAGCACAGC  
TCTCAGGGGGCAGTCAGGGACACTGGTCTTCCAGTGTAGCGTCCCAGCTTGGCTCTGTAAACAGACCTCT  
TTTGTTATGGATGGCTACAAAATAGGGCCCCAATGCTATTGTTTTTAAGTTGTTAAATTGTT  
AAGATTGCTAAGGCCAAAGGAATTGCGAAATCAAGTCTGTCAGTACAATAACATTAAAAGAAAATGGAT  
CCCACTGTTCTCTTGCACAGAGAACCCAGACGCCACAGGCTCTGCGCATTCAAAACAAACCATGAT  
GGAGTGGCGGCCAGTCCAGCCTTTAAAGAACGTCAGGTGGAGCAGCCAGGTGAAAGGCTGGGGAGGAAAG  
TGAAACGCCCTGAATCAAAGCAGTTCTAATTGACTTTAAATTTCATCCGGGGAGACACTGCTCCATT  
TGTGGGGGACATTAGCAACATCACTCAGAACGCTGTGTTCTCAAGAGCAGGTGTCTCAGCCTCACATGCCCT  
GCCGTGCTGGACTCAGGACTGAAGTGTGTAAGGAAGGAGCTGCTGAGAAGGACCACTCCACTGTGTGCCCTGGA  
GAATGGCTCTCACTACTCACCTGTCTTCAGCTCCAGTGTCTTGGGTTTTTAACTTTGACAGCTTTTT  
AATTGCATACATGAGACTGTGTTGACTTTTTAGTTATGTGAAACACTTGCCGAGGCCCTGGCAGAGGCA  
GGAAATGCTCCAGCAGTGGCTAGTGTCCCTGGTGTCTGCATGGCATCCTGGATGCTTAGCATGCAAGTTC  
CCTCCATCATTGCCACCTTGTAGAGAGGGATGGCTCCCCACCCCTAGCGTTGGGATTACGCTCCAGCCTCCT  
TCTTGGTTGTCTAGTGATAGGGTAGCCTTATTGCCCTCTTCTTAACTCCCTAAACCTCTACACTAGTGCCTA  
TGGGAACCAGGTCTGAAAAGTAGAGAGAAGTGAAGTAGAGTCTGGGAAGTAGCTGCTATAACTGAGACTAGA  
CGGAAAAGGAATACTCGTGTTAAGATATGAATGTGACTCAAGACTCGAGGCCGATACGAGGCTGTGATTCT  
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CTCATTATAAAAGCTTCAAAAAACCCA

## **FIGURE 124**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77624
><subunit 1 of 1, 310 aa, 1 stop
><MW: 35020, pI: 7.90, NX(S/T): 3
MALRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTSD
PRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLSKIWNVRRDSALYRCEVVARNDRK
EIDEIVIELTVQVKPVTPVCRVPKAHPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRA
NPRFRNSSFHLNSETGTLVFTAHKDDSGQYYCIASNDAGSARCEEQEMEVYDLNIGGIIGG
VLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRKSSFVI
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 243-263

**N-glycosylation sites.**

amino acids 104-107, 192-195

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 107-110

**Casein kinase II phosphorylation site.**

amino acids 106-109, 296-299

**Tyrosine kinase phosphorylation site.**

amino acids 69-77

**N-myristoylation sites.**

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267